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Minimum DB Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    1036.5
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Gapop 10.0., Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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    AAR91312
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AAW89329
AABB89453
AAB4790
AAM93206
                                                                                                                                                                                                                                                                                      SUMMARIES
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Human polypeptide
Human ORFX ORF1554
Human polypeptide,
Human polypeptide,
                                                                             N. gonorrhoeae gly
N. meningitidis Be
N. gonorrhoeae gly
Lipo-oligosacchari
Neisseria meningit
                                                                                                                                                                                                                        Description
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| 5 | 4 | w | 2 | _ | 0 | φ | œ | 7 | σ | G | 4 | w | N | 1 | 0 | 9 | æ | 7 | σ | υ | 4 | w | N | _ | 0 | 9 | œ | 7 | σ | Ų | 4 | w | N | _ |
|----------|----------|----------|----------|----------|----------|----------|----------|----------|--------------------|--------------------|----------|----------|----------|----------|--------------------|----------|----------|----------|--------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|----------|--------------------|--------------------|--------------------|--------------------|----------|----------|-------------------|
| C) | 86.5 | €. | S) | cη. | ₫. | €. | € | a) | σ ₁ | 87 | 88 | 88.5 | æ | S | 90 | 93.5 | 94 | tл | 95.5 | an. | ~ | æ | 99.5 | 105.5 | 106 | 119.5 | 119.5 | 119.5 | 119.5 | 121 | 129.5 | N | 129.5 | 129.5 |
| 5.9 | 5.9 | | | | | | | | | | | 6.1 | | | | | | | | | | | | | | | | | | | | | | 8.9 |
| 955 | 955 | 955 | 955 | 955 | 955 | 955 | 955 | 955 | 852 | 279 | 651 | 500 | 159 | 1378 | 261 | 444 | 739 | 389 | 161 | 578 | 273 | 273 | 273 | 168 | 201 | 622 | 622 | 622 | 521 | 1128 | 636 | 595 | 579 | 578 |
| 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 22 | 18 | 20 | 22 | 21 | 23 | 22 | 23 | 22 | 22 | 23 | 21 | 22 | 20 | 22 | 22 | 8T. | 23 | 22 | 22 | 21 | 22 | ນ | 21 | 20 | 22 |
| AAR42241 | AAR42240 | AAR42239 | AAR42238 | AAR42237 | AAR42236 | AAR42235 | AAR42234 | AAR42088 | ABG08255 | AAW21023 | AAY35171 | AAU27796 | AAB41784 | ABB57176 | ABG03682 | AAU76669 | ABB11417 | AAB82459 | AAE15943 | AAY97423 | AAB60321 | AAY32543 | AAB60317 | ABG22090 | AAW20604 · | ABP43477 | AAB88452 | AAM93427 | AAB41900 | АВВ62795 | ABP42016 | AAB12121 | AAY30812 | AAG81257 |
| p50 | p50 pro | | Novel human diagno | H. pylori cytoplas | ř | | | | Novel human diagno | | | s el | C38H2-2/141- | Rice 1-deoxy-D-xyl | Helicobacter pylor | H. pylori beta-1,4 | Helicobacter pylor | Novel human diagno | H. pylori cytoplas | secreted | | Human polypeptide, | Human ORFX ORF1664 | Drosophila melanog | Human ovarian anti | o . | secr | Human AFP protein |

ALIGNMENTS

N. gonorrhoeae glycosyltransferase LgtB.

Glycosyltransferase; lipo-oligosaccharide; lgt gene; LOS locus; vaccine.

RESULT 1
(AAR91312:
(AAR91312)
(AAR91312;
XX
AC AAR91312;
XX
DT 09-JUL-1996 (first entry)
XX
DT 09-JUL-1996 (first entry)
XX
Clycosyltransferase; lipo-oligosacchan
XX
Clycosyltransferase
Clyco Nucleic acids encoding glycosyl transferase(s) - used in the diagnosis of infection with Neisseria and for the biosynthesis oligo:saccharide(s)

of

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RESULT 2
AAY22156
  DT PI A XXX 
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Best Local S
Matches 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contg. activated Gal to an acceptor moiety comprising a GlcNAc or Glc residue in the presence of LgCB. Oligosaccharides can be produced that, when attached to non-toxic lipids, are useful for Neisseria vaccine prepn. Blood group core oligosaccharides, and mimics of lacto-N-neotetraose, gangliosides and saccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LgtB (AAR91312) can be obtd. by expression of the lgtB coding sequence in recombinant host cells. A method for adding Gal betal-4 to GlcNAc or Glc comprises contacting a reaction mixture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 Glycosyltransferases (AAT14061) of Neiserria
WPI; 1999-395174/33
                                                 Gilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                       saccharide donor; oligosaccharide synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beta-1,4-galactosyltransferase; lgtB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N. meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY22156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY22156 standard; Protein;
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15-DEC-1997;
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                                                                                                                                                                                                                                                                                 24-JUN-1999
                                                                                                                                                                                                                                                                                                                                WO9931224-A2
                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycosyltransferase;
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                                                                                                 (CANA )
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llarity 100.0%;
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97US-0069443.
                                                                                                                                                                                                                            98WO-CA01180
                                                                                                 COUNCIL CANADA.
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                                                                                                                                                                                                                                                                                                                                                                                                                               development.
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Mismatches 0;
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; nucleotide sugar formation;
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                                                                                                                          Glycosyltransferase; vaccine.
                                                                                                                                                                                                                                                                      AAR91315 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with a terminal galactose residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The fusion proteins are able to catalyse more than one reaction in the enzymatic synthesis. This is useful for the development of therapeutic agents that have specific carbohydrate structures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            accessory enzyme that is involved in formation of a nucleotide sugar which is a saccharide donor for a glycosyltransferase reaction. The fusion protein is useful in the enzymatic synthesis of oligosaccharides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        galactosyltransferase (also referred to as 1gtB). The invento a nucleic acid encoding a fusion protein that comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAX84281.
                                                                                           Neisseria gonorrhoeae strain F62
                                                                                                                                                                                                        09-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycosyltransferase catalytic domain and a catalytic domain
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                                                                                                                                                                       gonorrhoeae glycosyltransferase LgtE
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                                                                                                                                                                                                                                                                                                                                                                                                                                  VDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRRLNRKQQWRDS 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents
                                                                                                                                                                                                                                                                                                                                                    PANTFKHRLIRALTKISREREKRRQRREQ----FIVPFQ
                                                                                                                                                                                                                                                                                                                                                                                  PANTFKHRLIRALTKIGREREKRRORREQLIGKIIVPFQ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEKACFMSHAVLWKQALDEGLPYITVFEDDVLLGEGEEKFLAEDAWLQERFDPDTAFIVR 120
                                                                                                                                                                                                                                                                                                                                                                                                                VDLMMFSDFFDREGMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRLLNRKQQRRDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LETMFMHVLTSPSGVADYCGRAFPLLESEHWGTAGYIISRKAMRFFLDRFAALPPEGLHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycosyltransferase fusion esis of oligosaccharides
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                                                                                                                                                                                                        (first entry)
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90.0%;
                                                                                                                                         lipo-oligosaccharide;
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Pred. No. 3.4e-139;
7; Mismatches 17;
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                                                                                                                                         lgt gene;
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25-SEP-1995; 04-APR-1996 WO9610086-A1

95WO-US12317

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RESULT 4
AAWO650
ID AAWO
ID AAWO
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DT 21-b
DT Lipc
XX
DE Lipc
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DE N-ac
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Best Local S
Matches 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 Glycosyltransferases (AAR91311-15) are products of the 1gt (AAR714061) of Nelserria gonorrhoeae strain F62. Glycosyltrans LgtE (AAR91315) can be obtd. by expression of the 1gtE codding sequence in recombinant host cells. A method for adding Gal
                                                                               Polyglycosyltransferase; N-acetylglucosaminyl transferase; N-acetylgalactosaminyl transferase; lipo-oligosaccharide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     betal-4 to GlcNac or Glc comprises contacting a reaction mixture contg. activated Gal to an acceptor modety comprising a GlcNac or Glc. residue in the presence of LgtE. Oligosaccharides can be produced that, when attached to non-toxic lipids, are useful for Neisseria vaccine prepn. Blood group core oligosaccharides, and mimics of lacto-N-neotetraose, gangliosides and saccharide portions of globoglycolipids can also be produced using the enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis of infect:
oligo:saccharide(s)
 19-DEC-1996
                             WO9640971-A1
                                                                                                                            Lipo-oligosaccharide
                                                                                                                                                         21-MAR-1997
                                                                                                                                                                                    AAW06580;
                                                                                                                                                                                                             AAW06580 standard; Protein;
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                                                      Neisseria gonorrhoeae ATCC 33084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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)B; AAT14061.
                                                                                                                                                                                                                                                                                 ----RHRRSLKVMFDLKRALGKFGREKKKRMERQRQAELEKVYGRRVILFK
                                                                                                                                                                                                                                                                                                                                        VDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQNSMLGSDLEKDREQGR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.9%;
                                                                                                                                                                                                                                                                                                   -LIRALTKIGREREKRRQRR-----EQLIGKIIVPFQ
                                                                                                                            gene-encoded protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                              280 AA
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Pred. No. 2.8e-110;
4; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 products of the lgt locus
in F62. Glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transfer of at least 2 saccharide units using poly:glycosyl:transferase - isolated from N. gonorrhoeae, the addition of both GlcNac and GalNac di:saccharide(s) un
                                                             Neisseria meningitidis
                                                                                   glycosyltransferase;
                                                                                            Neisseria meningitidis; lgtC; lgtB; beta-1,4-galactosyltransferase
                                                                                                                  Neisseria meningitidis lgtB C-terminal peptide
                                                                                                                                         26-FEB-1999
                                                                                                                                                            AAW89328;
                                                                                                                                                                                   AAW89328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
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                                         WO9854331-A2
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                                                                                                                                                                                                                                                                                                                                                                       VEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLAEDTWLEERFDKDSAFIVR
                                                                                                                                                                                                                                                                                                                                                                                 VEKACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSAFVVR
                                                                                                                                                                                                                                                           PANTFKHR------LIRALTKIGREREKRRQRR-----EQLIGKIIVPFQ
                                                                                                                                                                                                                                                                                                                            LETMFAKVIVRPDFVLNYENRSFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKA
                                                                                                                                                                                                                                                                                 VDLMMFTYFFDLEGMPVYQVSPALCTQELHYAKFLSQNSMLGSDLEKDREQGR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           galactose moiety
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 71.0
                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                       -RHRRSLKVMFDLKRALGKFGREKKKRMERQRQAELEKVYGRRVILFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the specification
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                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnson
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                                                                                                                                                                                  peptide;
                                                                                   proteolytic enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.6%;
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Pred. No. 1.1e
23; Mismatches
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1.1e-109;
hes 35; I
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26-MAY-1998; 03-DEC-1998

98WO-IB00975

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RESULT 6
AAW89329
ID AAW89329
ID AAW8
XX AAW8
AC AAW8
AC AAW8
XX Neis
KW Neis
KW 91yc
XX Neis
KW 92yc
XX Neis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A method has been developed of expressing a glycosyltransferase in a host cell. The method comprises introducing into the host cell a nucleic acid encoding the glycosyltransferase and incubating the host cell under conditions appropriate for expression of the glycosyltransferase, where the host cell substantially lacks a protease that cleaves polypeptides between two consecutive positively charged amino acid residues. The glycosyltransferase can be used in in vitro production of oligosaccharide structures which are potential therapeutic agents for use in the manipulation of cell-cell recognition events, particularly adhesion of bacteria and viruses to mammalian cells and leukocytenendothelial cell interaction through selectins in inflammation. The method provides more readily recoverable active glycosyltransferases. The
Expressing high levels of glycosyltransferases either host cells deficient in proteolytic enzy
                                                                                 WPI; 1999-035177/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis; lgtC; lgtB; beta-1,4-galactosyltransferase; glycosyltransferase; proteolytic enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence represents a C-2 manual peptide meningitidis lgtB from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycosyltransferase genes deleted
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                                                                                                                                                                                                                                                                                                                                                                                                                       WO9854331-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAY-1997;
                                                                                                                                     Wakarchuk WW,
                                                                                                                                                                                                                                                                                                           26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                               03-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW89329 standard;
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                                                                                                                                                                                          (CANA ) NAT RES COUNCIL CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CANA ) NAT
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46; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    meningitidis lgtB C-terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50
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                                                                                                                                                                                                                                                 97US-0047751.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide;
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85.2%;
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Pred. No. 2e-17;
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comprises use
s or modified
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Matches
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                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                           method provides more readily recoverable active glycosyltransferases than prior art methods involving mammalian glycosyltransferases. The present sequence represents a C-terminal peptide from Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A method has host cell. Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycosyltransferase genes deleted in
                                                                                                                                                                                                                                                                                                                                                      meningitidis lgtB
226 EHDRRLNRKQQWRDSPANTFKHRLIRALTKIGREREKRRQRREQLIGKIIVPFQ
                                                                                                                                                      Local
                                                                                                                      1 Similarity
45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Fig 8;
                                                                                                                                                                                                                                                                                 50 AA;
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        been developed of expressing a glycosyltransferase he method comprises introducing into the host cell a
                                                                                                                                                                                                                                                                                                                                                      from the present invention.
                                                                                                                                                  14.9%;
                                                                                                              Score 217; DE Pred. No. 3.4e 0; Mismatches
                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a proteolytic recognition site
                                                                                                              DB 20;
1.4e-17;
les 5;
                                                                                                                                                                                       Length 50;
                                                                                                                  Indels
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                                                                                                              Gaps
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ABB89453
                                                                                                                      RESULT 7
Human polypeptide
                              24-MAY-2002
                                                            ABB89453
                                                                                         ABB89453 standard; Protein; 423
                                                                                                                                                                  \vdash
                                                                                                                                                                  EHDRLLNRKQQWRDSPANTFKRRLIRALTKISREREIRRQRREQ----FIVPFQ
                            (first entry)
 SEQ ID NO 1829
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Cytostatic; immunosuppressive; nootropic; antiallergic; hepatotropic; antidiabetic; vulnerary; anticonvulsant; antibacterial; neurological Homo sapiens. gene therapy; disease; infection; human; secreted protein. cancer; disorder; neuroprotective; antiviral; antiinflammatory; antiulcer; antifungal; antiparasitic; cardiovascular disorder;

WO200190304-A2

29-NOV-2001

18-MAY-2001; 2001WO-US16450

19-MAY-2000; 2000US-205515P

(HUMA-) HUMAN GENOME SCI

CE, Rosen CA

WPI; 2002-122018/16

Novel 1405 isolated polypeptides, useful for diagnosis, prevention of neural, immune system, muscular, reproduct gastrointestinal, pulmonary, cardiovascular, renal and p N-PSDB; ABL89862 reproductive, treatment and

proliferative

gastrointestinal, disorders -

Claim 11; SEQ ID NO 1829; 2081pp + Sequence Listing; English

The invention relate (ABB89040-ABB90444) relates to es to novel useful for genes (ABL89449-ABL90853) preventing, treating or an ameliorating

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AAB41790
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Best Local
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                                                                                                                                                                                                                                                                                                                                              Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulsant; otherably; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension, neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bond dispersional anaemia; nocturnal haemoglobinuria; burn; wound; continuing continuing the continuing continuing continuing the continuing continuin
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format direction wipo int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ORFX ORF1554 polypeptide sequence SEQ
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05-OCT-2000
                                                                                      WO200058473-A2
                                                                                                                                                                                                                                                                                                                           bone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVVRLETMEMHVLTSP-SGVADYGGR--AFPLLESEHCGTAGYIIS-----RKAMRFF 166
                                                                                                                                                                                                                                                                                                             damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRGRLERLMEDVEAEKLSWDLIYLGRKQVNPEKETAVEGLPGLVVAGYSYWTLAYALRLA
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                                                                                                                                                                                                                                                                                                                 cartilage damage;
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Pred. No. 9.3e-06;
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31-MAR-2000; 2000WO-US08621

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RESULT 9
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatclogical; immunosuppressive; antidiabetic; hypotensive; dermatclogical; immunosuppressive; antifilammatory; antibacterial; antiviral; antifungal; antirherantithurgal; antirherantithurgal; antirheranticuls; antiparticuls; antiparticuls; antirheranticuls; antiparticuls; antirheranticuls; antiparticuls; antipart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                      Human polypeptide, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reduciel acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, thypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 2331-2332; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                  06-NOV-2001
                                                                                                                                                                                                      AAM93202 standard; Protein; 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              allergies, aplastic anaemia, burns, wounds, bone and cartilage on nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    f: | ||:|| :||: : |: : |||||||
TLTKGEVGCFLSHYSIWEEVVARGLARVLVFEDDV-
                                                                                                                                                                                                                                                                                                                                                       GARKLLASQPLRRMLPVDEFLPIMFDQHPNEQYKAHFWPRDLVAFSAQPLLAA-PTHYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LSGVEKACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VISLARRPDRRERMLASLWEMEISGRVVDAVDGWMLNSSAIRNLGVDLLPGYQ-DPYSGR 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRGRLERLMEDVEAEKLSWDLIYLGRKQVNPEKETAVEGLPGLVVAGYSYWTLAYALRLA
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                                                                              (first entry)
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Pred. No. 1.3e-05;
                         2591
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RESULT 10
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Best Local
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          Human polypeptide,
                                  06-NOV-2001
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11-JAN-2000;
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                                                                            AAM93206 standard;
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                                                                                                                                                                                                                            305 TLTKGEVGCFLSHYSIWEEVVARGLARVLVFEDDV-----
                                                                                                                                                                                                                                                                        246 VISLARRPDRRERMLASIWEMEISGRVVDAVDGWMLNSSAIRNLGVDLLPGYQ-DPYSGR 304
                                                                                                                                                                                                                                                   58 -LSGVEKACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSA 116
                                                                                                                                                                                                                                                                                                                      Local Similarity
les 65; Conser
                                                                                                                                                                                                                                                                                               5 VISLASAAERRAHIAATFGSRGIPFQFFDA----LMPSERLERAMAELVPGLSAHPY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDR--FAVLPPERLHPVD----LMMFGNPDDR-----EGMPVCQLNPALCAQELHYA 212
                                                                                                                                    GARKLLASQPLRRMLPVDEFLPIMFDQHPNEQYKAHFWPRDLVAFSAQPLLAA-PTHYA
                                                                                                                                                                                 FRGRLERLMEDVEAEKLSWDLIYLGRKQVNPEKETAVEGLPGLVVAGYSYWTLAYALRLA
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                                                                                                                                                                                                                                                                                                                                                                 517 AA;
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2000JP-0118774.
2000JP-0183765.
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                                                                            Protein;
           SEQ ID
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                                                                                                                                                                                                                                                                                                                              8.9%;
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a T, Nagai K, Kojima
           NO:
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Pred. No. 1.3e-05;
0; Mismatches 91;
           2599
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S, Otsuki T,
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Best Local Similarity
         Human AFP protein sequence
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11-JAN-2000;
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                               10-SEP-2001
                                                      AAG81257;
                                                                                                                                                                                                                                                                                                                                                              Sequence
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N-PSDB; AAK94114.
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GXAX FX GX

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SEQ ID NO:32

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molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      830 Primers useful for synthesizing full length cDNA use in genetic manipulation - \,
AAG81257 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to primers for synthesising full length clones. 830 cDNA molecules encoding a human protein have been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID NO 2599; 1380pp + sequence listing; English
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                                                                                                                                                      GARKLLASQPLRRMLPVDEFLPIMFDQHPNEQYKAHFWPRDLVAFSAQPLLAA-PTHYA 462
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                                                                                                                                                                                                                                                                                                                                             FVVRLETMEMHVLTSP-SGVADYGGR--AFPLLESEHCGTAGYIIS-----RKAMRFF 166
                                                                                                                                                                                                                                                                                                                                                                                                               TLTKGEVGCFLSHYSIWEEVVARGLARVLVFEDDV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LSGVEKACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSA 116
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2000JP-0183765
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27.2%;
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a T, Nagai K, Kojima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 129.5; DB 22;
Pred. No. 1.3e-05;
"" matches 91;
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S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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T, Ko
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RESULT 12
AAY30812
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                            Secreted protein; prevention; treatment; protein therapy; gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; blood disorder;
                                                                                                             Human
                                                                                                                                                                   12-OCT-1999
                                                                                                                                                                                                                        AAY30812;
                                                                                                                                                                                                                                                                        AAY30812 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OMYZ)
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                                                                                                                                                                                                                                                                                                                                                                                                               483
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                                                                                                                                                                                                                                                                                                                                                                                                         GARKLLASQPLRRMLPVDEFLPIMFDQHPNEQYKAHFWPRDLVAFSAQPLLAA-PTHYA 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLTKGEVGCFLSHYSIWEEVVARGLARVLVFEDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VISLARRPDRRERMLASLWEMEISGRVVDAVDGWMLNSSAIRNLGVDLLPGYQ-DPYSGR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDR--FAVLPPERLHPVD----LMMFGNPDDR-----EGMPVCQLNPALCAQELHYA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRGRLERLMEDVEAEKLSWDLIYLGRKQVNPEKETAVEGLPGLVVAGYSYWTLAYALRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVVRLETMFMHVLTSP-SGVADYGGR--AFPLLESEHCGTAGYIIS-----RKAMRFF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-300340/31.
                                                                                                             secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 121-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       578 AA;
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                                                                                                                                                                   (first
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  abnormality;
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neurodegenerative disorder; fetal deficiency; leukemia;
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Pred. No. 1.5e-05;
0; Mismatches 91
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                                                                                                          gene
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leukemia; autoimmune; acne,
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Best
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09-FEB-1998;
09-FEB-1998;
09-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel isolated human genes and the secreted proteins they encode. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for the polynucleotides of the invention based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and fetal deficiencies, blood disorders, leukemias,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, obesity, osteoporosis, arthritis, infections, AIDS, connective tissue disorders, transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hepatic disease; renal disease; lymphoma; inflammation; allergy; as Alzhelmer's disease; cognitive disorder; schizophrenia; obesity; see osteoporosis; arthritis; infection; AIDS; connective tissue disorder transplant rejection; diabetes; psoriasis; cardiovascular disorder; reproductive disorder; food additive; food preservative; human; pri
                                                                                                                                                                                                                                                                                                                                                                                                                                    reproductive disorders. The polypeptides or polynucleotides can also used as food additives or preservatives. The polypeptide are also use for identifying their binding partners. This sequence represents a secreted protein described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human genes potentially abnormalities and fetal deficiencies
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                                                                                                                            FRGRLERLMEDVEAEKLSWDLIYLGRKQVNPEKETAVEGLPGLVVAGYSYWTLAYALRLA
                                           FVVRLETMFMHVLTSP-SGVADYGGR--AFPLLESEHCGTAGYIIS-----RKAMRFF 166
                                                                                              TLTKGEVGCFLSHYSIWEEVVARGLARVLVFEDDV
                                                                                                                                                                                         VISLARRPDRRERMLASLWEMEISGRVVDAVDGWMLNSSAIRNLGVDLLPGYQ-DPYSGR 382
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65; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 206-208; 263pp; English.
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98US-0074037.
98US-0074118.
98US-0074141.
98US-0074157.
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sepsis;
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                                                           Query Match
Best Local Similarity
                                                                                                                                                                                            Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophylaxis of cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is a human protein which has at least one hydrophobic domain. This protein may be a secretory or a membrane protein. The present protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoiesis activity, tissue growth activity, haemostatic activity, chemotactic/chemokinetic activity, haemostatic
                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                          Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       blophylaxis; signal receptor; ion channel; transporter; immunostimulant; immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.
                                                                                                                                                and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present protein could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-1998;
22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200029448-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrophobic domain protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB12121
                                                                                                                                                                                                                                                                                                                                                                                             activities e.g. immunomodulatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proliferation control; differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PROT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SAGA )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L6-MAR-1999;
27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  483 GARKLLASQPLRRMLPVDEFLPIMFDQHPNEQYKAHFWPRDLVAFSAQPLLAA-PTHYA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167
5 VISLASAAERRAHIAATFGSRGIPFQFFDA----LMPSERLERAMAELVPGLSAHPY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-387753/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDR--FAVLPPERLHPVD----LMMFGNPDDR-----EGMPVCQLNPALCAQELHYA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA60183, AAA60193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAGAMI CHEM RES CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kimura T;
                                                                                                                                       and cancer
                                                                                                                                                                                                                                                                                                                                                Page 184-186; 410pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                       595 AA;
                                             8.9%; ilarity 27.2%; Conservative
                                                                                                                                                                                                                                                                                                                                                                               thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99JP-0069811.
99JP-0119299.
99JP-0138169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-0326255.
98JP-0364315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-JP06412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane
                                               30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         595
                                            Score 129.5; DB 21
Pred. No. 1.5e-05;
0; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone HP02962 isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                          antiinflammatory, chemokinetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    induction; material transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hydrophobic
                                                                         21;
                                               Indels
                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    doma
                                             53;
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                                            Gaps
                 57
                                             12;
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RESULT 14
ABP42016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XHXA
                            recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation,
                                                                                                                                                         The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to
                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disoorderian cancer; breast cancer; anovulation; polycystic ovary infertility; pregnancy disorder; anovulation; polycystic ovary
polycystic ovary syndrome, disorders, infections (e.g
                                                                                                                                                                                                                                                        Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200200677-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastrointestinal disorder; urinary system disorder; drug
gene therapy; chromosome mapping; forensic analysis;
antibody preparation; cytostatic; immunomodulatory; neuro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurologi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP42016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP42016 standard; Protein; 636
                                                                                                                                                                                                                                                                                           neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58
                                                                                                                                                                                                                                                                                                                                                                                    2002-147878/19
)B; ABQ55093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GARKLLASQPLRRMLPVDEFLPIMFDQHPNEQYKAHFWPRDLVAFSAQPLLAA-PTHYA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VISLARRPDRRERMLASLWEMEISGRVVDAVDGWMLNSSAIRNLGVDLLPGYQ-DPYSGR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDR--FAVLPPERLHPVD----LMMFGNPDDR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLTKGEVGCFLSHYSIWEEVVARGLARVLVFEDDV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRGRLERLMEDVEAEKLSWDLIYLGRKQVNPEKETAVEGLPGLVVAGYSYWTLAYALRLA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVVRLETMFMHVLTSP-SGVADYGGR--AFPLLESEHCGTAGYIIS-----RKAMRFF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LSGVEKACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSA 116
                                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-209467P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-US18569.
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                                                                                                                                                                                                                                                        IJ
                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gynaecological; reproductive
                                                                                                                                                                                                                                                       3148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HFKHF51,
                                                                                                                                                                                                                                                       2922pp;
               ovarian cysts,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunomodulatory; neuroprotective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO:3148
                 and dysmenorrhoea),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -EGMPVCQLNPALCAQELHYA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RF--ESN 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorder;
                 endocrine
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is

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RESULT 15
ABB62795
ID ABB62
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                      23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
  New isolated nucleic acid genes from Drosophila and
                                                                                             WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                            27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                          WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 15177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and urinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       shock syndrome),
vaginitis), immur
                                                                       N-PSDB; ABL06898
                                                                                                                                              Venter JC,
                                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB62795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB62795 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  respiratory disorders, neurological disorders, gastrointestinal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             blood-related disorders
                                                                                                                                                                                       (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotides may also be used in screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nmunodeficiencies, autoimmune oophoritis, systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 524 GARKLLASQPLRRMLPVDEFLPIMFDQHPNEQYKAHFWPRDLVAFSAQPLLAA-PTHYA 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 VISLASAAERRAHIAATFGSRGIPFQFFDA----LMPSERLERAMAELVPGLSAHPY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        itp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLTKGEVGCFLSHYSIWEEVVARGLARVLVFEDDV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VISLARRPDRRERMLASLWEMEISGRVVDAVDGWMLNSSAIRNLGVDLLPGYQ-DPYSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -LSGVEKACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDR--FAVLPPERLHPVD----LMMFGNPDDR-----EGMPVCQLNPALCAQELHYA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRGRLERLMEDVEAEKLSWDLIYLGRKQVNPEKETAVEGLPGLVVAGYSYWTLAYALRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVVRLETMEMHVLTSP-SGVADYGGR--AFPLLESEHCGTAGYIIS-----RKAMRFF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                            CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              636 AA;
                                                                                                                                           Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ome), inflammatory conditions (e.g., mastitis, or immune disorders (e.g., congenital and acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                            NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.9%;
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                                                                                                                                           PWD,
detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences (ABL01840 (ABB57737-ABB72072)
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APPLICANT: Gotschli
TITLE OF INVENTION:
TITLE OF INVENTION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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APPLICATION NUMBER: (
FILING DATE: Septembe
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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STATE: New Jersey
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VENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS
VENTION: OLIGOSACCHARIDES, AND GENES ENCODING
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Pred. No. 4.1e-160;
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Patent No. 5798233
Patent No. 5798233
Patent No. 5798233
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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RECISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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PRIOR APPLICATION DATA:
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TELEPHONE: 201 343-1684
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                LETMFMHYLTSPSGVADYGGRAFPLLESEHCGTAGYIISRKAMRFFLDRFAVLPPERLHP 180
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VENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
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Pred. No. 4.1e-160;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
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PRIOR APPLICATION NUMBER:
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
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                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
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GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
OLIGOSACCHARIDES, AND GENES ENCODING THEM
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Pred. No. 4.1e-160;
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Best Local Similarity
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/33,412
FILING DATE: 15-Jun-1999
CLASSIFICATION: - CURKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
                                                                                                                                            VEKACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSAFVVR 120
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VDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRRLNRKQQWRDS
              VDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRRLNRKQQWRDS
                                                                             LETMFMHVLTSPSGVADYGGRAFPLLESEHCGTAGYIISRKAMRFFLDRFAVLPPERLHP
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                                                             LETMFMHVLTSPSGVADYGGRAFPLLESEHCGTAGYIISRKAMRFFLDRFAVLPPERLHP
                                                                                                                           VEKACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSAFVVR 120
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                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 279 amino acids
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STREET: 411 Hackensack Avenu
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Pred. No. 4.1e-160;
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               Matches
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INFORMATION FOR SEQ ID NO:
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
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                                PANTFKHR------LIRALTKIGREREKRRQRR-----EQLIGKTIVPFQ 279
                                                                                   VDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRRLNRKQQWRDS 240
                                                                                                                                  VEKACFMSHAVLMEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSAFVVR 120
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                                                                VDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQNSMLGSDLEKDREQGR----
----RHRRSLKVMFDLKRALGKFGREKKKRMERQRQAELEKVYGRRVILFK 280
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RESULT 7

RESULT 8 US-08-683-458-6

Sequence 6, Application US/08683458 Patent No. 5798233

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Best Local Similarity 71.6%;
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acids
TOPOLOGY: 11--
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MEDIUM TYPE: Floppy disk
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REFERENCE/DOCKET NUMBER: 600
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                             PANTEKHR------LIRALTKIGREREKRRQRR-----EQLIGKIIVPFQ 279
                                                            VDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQNSMLGSDLEKDREQGR-----
                                                                                         VDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRRLNRKQQWRDS 240
                                                                                                                        LETMFMHVLTSPSGVADYGGRAFPLLESEHCGTAGYIISRKAMRFFLDRFAVLPPERLHP 180
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VENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
VENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
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ber 26, 1994
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Pred. No. 3.4e-111;
Prematches 34;
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                Sequence 6, Application US/08878360 
Patent No. 5945322 
GENERAL INFORMATION: 
APPLICANT: Gotschlich, Emil C.
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Best Local 9
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT: Gotschli
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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ADDRESSEE: Klauber & Jackson
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                                                                                                                                                       PANTFKHR------LIRALTKIGREREKRRQRR-----
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r: Gotschlich, Emil C.
INVENTION: GLYCOSYLTRANSFERASES
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GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
OLIGOSACCHARIDES, AND GENES ENCODING THEM
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RESULT 10 US-08-478-140B-6

Sequence 6, Application US/08478140B Patent No. 6127153
GENERAL INFORMATION:

APPLICANT: APPLICANT:

BUCZALA,

ROTH, STEPHEN

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Best Local Similarity 71.6
Matches 209; Conservative
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MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES:
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                  241 PANTFKHR------LIRALTKIGREREKRRORR-----EQLIGKIIVPFQ 279
234
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FILING DATE: 18-JUN-1997
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REGISTRATION NUMBER: 26,742
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----RHRRSLKVMFDLKRALGKFGREKKKRMERQRQAELEKVYGRRVILFK 280
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; Pred. No. 3.4e-111;
24; Mismatches 34;
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                                                                         Sequence 6, Application US/U9333412
Patent No. 6342382
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,140B
FILING DATE: 07-JUN-1995
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ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 3
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Local Similarity 71.6%;
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                                             INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF OLIGOSACCHARIDES, AND GENES ENCODING THE
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Pred. No. 3.40
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; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-333-412-6
                                                                                                                                                Patent No. 6379933
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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TITLE OF INVENTION:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn R
CURRENT APPLICATION DATA:
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LENGTH: 280 amino acids
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                                                                                                                                                                                                                                                                                                                           MONHVISLASAAERRAHIADTFGSRGIPFQFFDALMPSERLEQAMAELVPGLSAHPYLSG
                                                                                                                                                                                                                                                                                                                                                                                                             VDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRRLNRKQQWRDS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LETMFMHYLTSPSGVADYGGRAFPLLESEHCGTAGYIISRKAMRFFLDRFAVLPPERLHP 180
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                                                                                                                                                                        , Application 6379933
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ULE TYPE: protei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 411 Hackensack Avenue CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 26, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                           BUCZALA, STEPHANIE L.
VENTION: METHOD OF TRANSFERRING AT LEAST TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                        ROTH,
                                                                                                                          JOHNSON, KARL F.
                                                                                                        STEPHEN
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71.6%;
  POLYGLYCOSYLTRANSFERASE
                 SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE, POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
                                                                                                                                                                                            US/09338943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1036.5; DB 4
Pred. No. 3.4e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          600-1-095
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RESULT 13
US-08-701-191A-27
; Sequence 27, Application US/08701191A
; Patent No. 5942428
; Patent No. 5942428
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Matches
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                       GENERAL INFORMATION:
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REFERENCE_DOCKET NUMBER: 718
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acid
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                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                        APPLICANT: MOOSA MOhammadi, Joseph Schlessinger,
APPLICANT: and Stevan R. Hubbard
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
TITLE OF INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             241 PANTFKHR-----LIRALTKIGREREKRRORR-----EQLIGKIIVPFQ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 VDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRRLNRKQQWRDS
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                          STREET:
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                                               ADDRESSEE:
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10036-2711
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1155 Avenue of the Americas
E: Lyon & Lyon 633 West Fifth Street Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.9%; Score 1036.5; DB 4; 71.6%; Pred. No. 3.4e-111; rive 24; Mismatches 34;
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; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3799
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Best Local S
Matches 35
                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: LYNN DOUCETTE-Staimm et al
TITLE OF INVENTION: NUCLEIC ACID AND
TITLE OF INVENTION: EPIDERMIDIS FOR
                                                 PRIOR FILING DATE: 1997-08
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3799
LENGTH: 337
                                                                                                                                                                                                                                                                                                           Sequence 3799, Application US/09134001C Patent No. 6380370
                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
                                                                                                                        PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                   FILE REFERENCE: GTC-007
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NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
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MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            163
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                                                                                                                                                                                                                                                                                                                                                                                                                          240 ----NPYPGIPPERL--FNLLKTGHRMER----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 DSAFVVR------LETMFMHVLTSPSGVADYGGRAFPLLESEHCGTAGYIISRKA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 ERALTMGDLISFAWQISQGMQYLAEMKLVHRDLAARNILVAEGRKMKISDFGLSRDVYEE 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM CO
OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 EKACFMSHAVLWEQALDEGVPYIA----VFED----DVLLGEGAEQFLAEDTWLQERFDP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 304 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRFFLDRFAVLPPERLHPVDLMMFGNPDDREGMPVCQLNPALCAQELH 210
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California
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(OK: 530
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                                                                                                        1997-08-14
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; ORGANISM: Synechocystis sp.
US-09-564-805-236
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US-09-564-805-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PA
SEQ ID NO 236
• LENGTH: 554
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 21.5
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 200 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/564,805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICANT: Rommens, Johanna M.
PPLICANT: Myriad Genetics, Inc.
ITLE OF INVENTION: Chromosome 17p-Linked F
ITLE OF INVENTION: Gene and a Paralog and
415 AAGNAVALPIGDRFVQPTPPPPQIYEGEIHELEPNKQIHHLGEVVIHLDGQILENSRW 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 LAEDTWLQERFDPDSAFVVRLETMFMHVLTSPSGVADYGGRAFPLLESEHCGTAGYIISR 160
                                                                               363 YLLADHSDGRNTTQLIHN----LRPQHL----VFVHGQPSDIEDLTSLEELQSRYQLHSP 414
                                                                                                                          151 CGTAGYIISRKAMRFFLDRFAVLPPERLHPVDLMMFGNPDDREGMPVC-----QLN-- 201
                                                                                                                                                                                                                                                    250 LWAGESVARGCDAYQGIIDHLPDNVRNFAQHQPLFWD---DKVYPHLRPLTDD--QGELS 304
                                                                                                                                                                                                                                                                                                                                      191 YGNRRLPHRRQQEKQFIQAIETVLAKGRNILLPVPPLGLAQ-EILKLLRTHHQFTGRQVN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 KAMRFFLDRFAVLPPERLHPVDLMM-----FGNPDDREGMPVCQLN 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 IATETEMQ-----AFLNLPKTLFKN-----EKARKSILILQKKKSG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 IMHHLIEVDPVLSRVSVHLANF--LEIPFDVYPQDAIMP---LPLEEADVVIGDFPIGYY 204
                                                                                                                                                                                                                                                                                            61 -----VEKAC-------FMSHAVL-WEQALDEGVPYIAVFEDDVLLGE-- 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 P-----YLSGVEKACFMSHAVLWEQALD----EGVPYIAV----FEDDVLLGEGAEQF 100
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                                                                                                                                                                    LSAPSIVITTW--PAFWPSPAALPGLWTVFMPQLLTLPSCLVNFAWQDLEEFPKYELED 362
                                                                                                                                                                                            -GAEQFLAEDTWLQERFDPDSAFVVRLETMFM-HVLTSPSGVADYGGR---AFPLLESEH 150
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                                     ------PALCAQELHYAKFHDQNSALGSLIEH-DRRLNRKQQW 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.6%; Score 81.5; DB 4; Length 337; 22.1%; Pred. No. 0.52; ative 39; Mismatches 64; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                           5.5%; Score 81; DB 4; Length 554; 21.5%; Pred. No. 1.3; ative 37; Mismatches 99; Indels
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RER: US 60/107,468
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Search completed: May 27, 2003, 18:18:46
Job time: 30 secs

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Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published_Applications_AA: *
                                                                                                                                                                                                                                                                                                                                                                                                                             : /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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 US-10-218-381-1

US-10-235-056-7

US-09-895-913A-186

US-09-988-626-236

US-09-988-626-236

US-09-988-626-236

US-09-988-626-236

US-09-988-626-236

US-09-988-626-236

US-09-864-761-48086

US-10-235-056-11

US-10-235-056-11

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US-10-235-056-11

US-09-849-031A-1

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10 US-09-815-242-5371

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US-09-211-691-2
US-10-007-267-6
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Sequence 8, Appli
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Sequence 186, Appli
Sequence 186, Appli
Sequence 236, Appli
Sequence 236, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 22, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 24, Appli
Sequence 27, Appli
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US-10-007-267-8
; Sequence 8, Application US/10007267
; Patent No. US20020127682A1
; GENERAL INFORMATION:
                              TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/312,387
FILING DATE: July 7, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Ver CURRENT APPLICATION UNMBER: US/10/007,267 FILING DATE: 03-Dec-2001 CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION NUMBER: US/09/333,412 FILING DATE: 15-Jun-1999
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.
72
72
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gotschlich,
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Hackensack
STATE: New Jersey
                                                                           TELEFAX: 201 343-1684
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               279 amino acids
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0 US-09-815-242-10734

0 US-09-739-451-4

US-10-097-065-137

0 US-09-739-451-12

0 US-09-737-149-30

0 US-09-737-149-30
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US-10-166-087-34
US-09-738-626-5823
US-09-764-868-826
US-10-029-115-4
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US-10-097-340-208
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US-09-789-390-13
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US-10-034-623-4

US-10-027-801-4
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                                                                                                                                                                                                                                                                                                            Version #1.25
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Sequence 4773, Ap
Sequence 5, Appli
Sequence 208, App
Sequence 208, App
Sequence 5004, App
Sequence 10734, Ap
Sequence 1,7, App
Sequence 137, App
Sequence 12, Appli
Sequence 12, Appl
Sequence 25, Appl
Sequence 30, Appl
Sequence 30, Appl
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Sequence 5823
Sequence 826,
Sequence 4, A
Sequence 2,
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Sequence 4, A
Sequence 4, A
Sequence 4, A
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Database

Post-processing: Minimum Match
Maximum Match

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB Maximum DB

seq length: 0 seq length: 2000000000

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34, Appl
5823, Ap
826, Appli
4, Appli
ee 2, Appli
13, Appl
11, Appl

1, Appli 17, Appl 4, Appli 4, Appli 4, Appli 4, Appli

Scoring table: Sequence:

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Gapop 10.0 , Gapext 0.5

Perfect score:

US-10-007-267A-8 1461

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; SEQUENCE DESCRIPTION: SEQ ID
US-10-007-267-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               us-09-211-691-2
                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/211,691
CURRENT FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 'US 60/069,443
PRIOR FILING DATE: 1997-12-15
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                   Query Match
Best Local
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TYPE: PRT
ORGANISM: Neisseria meningitidis
-09-211-691-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Fusion Proteins
TITLE OF INVENTION: Oligosaccharides
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APPLICANT:
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181 VDLMMFSDFFDREGMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRLLNRKQQRRDS
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                                  181 VDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRRLNRKQQWRDS 240
                                                                                                                                    61
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                                                                                                                                   VEKACFMSHAVLWKQALDEGLPYITVFEDDVLLGEGEEKFLAEDAWLQERFDPDTAFIVR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEKACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSAFVVR 120
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Wakarchuk, Warren W.
National Research Council of Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gilbert, Michel
                                                                                                                                                                                                                                                                    Conservative
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019957-012910US
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90.0%;
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Pred. No. 4.6e-125;
7; Mismatches 17;
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Pred. No. 6.2e-143;
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Patent No. US20020127682A1
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                             Matches
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INFORMATION FOR SEQ ID NO: 6:
     181
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                                                                                                                                               61
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NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-095

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
APPLICATION NUMBER: 08/312,387
FILING DATE: July 7, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Klauber & Jackson
                        VDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRRLNRKQQWRDS
                                                                                         LETMFMHVLTSPSGVADYGGRAFPLLESEHCGTAGYIISRKAMRFFLDRFAVLPPERLHP 180
                                                                                                                                                                VEKACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQEFFDPDSAFVVR 120
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                                                                      LETMFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIISREAMRFFLDRFAVLPPERIKA 180
                                                                                                                                             VEKACFMSHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLAEDTWLEERFDKDSAFIVR
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VDLMMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQNSMLGSDLEKDREQGR------
                                                                                                                                                                                                                                                                                             209;
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/007,267 FILING DATE: 03-Dec-2001 CLASSIFICATION: <Unknown>
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 280 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                             Conservative
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INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07601
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                                                                                                                                                                                                                                                                                                              70.9%;
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                                                                                                                                                                                                                                                                                          Score 1036.5; DB
Pred. No. 4.7e-99;
04; Mismatches 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-218-381-1
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US-10-235-056-7
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                  PRIOR FILING DATE: 1999
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn vers
SEQ ID NO 7
LENGTH: 389
TYPE: PRT
                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/10235056 Publication No. US20030059915A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.7%; score 98.5; Best Local Similarity 23.9%; Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/JP99/00321
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: JP 10-023389
PRIOR FILING DATE: 1998-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: GLYCOSYLTRANSFERASE AND DNA ENCODING THE SAME FILE REFERENCE: 2139.18
CURRENT APPLICATION NUMBER: US/10/218,381
CURRENT FILING DATE: 2002-08-15
                                                                                                                 CURRENT APPLICATION NUMBER: US/10/235,056
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: US 09/461,321
PRIOR FILING DATE: 1999-12-15
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                                                                                                                                                                                                                    APPLICANT: Ju, Tongzhong
TITLE OF INVENTION: CORE 1 3-GALACTOSYL TRANSFERASES
                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                            APPLICANT: Canfield, William M. APPLICANT: Cummings, Richard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                                     FILE REFERENCE: 5820.630
ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                               200 AKVE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 MRFFLDRFAVLPPERLH-----PVDLMM 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 YVRL----MHLLYDPNVKSE-----PLNHKNHEIQERVGIIKAYSHGVGTQGYVITPKI 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 MSLGELGCYASHYSLWEKCIELN-EAICILEDDITLKEDFKEGL---DFLEKHI--QELG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 -----ACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSAF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 QIFDAIY-SKTFEGGLHPLVK-KHLHPYFITQNIKDMGITTNLISEVSKFYYALKYHAKF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 QFFDALMPSERLERAMAELVPGLSAHPY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/601,519 FILING DATE: 2000-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVRLETMEMHVLTSPSGVADYGGRAFPLLESEH-----
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Akio OZAKI
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                                                                             version 3.1
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TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-895-913A-186
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                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/895,913A CURRENT FILING DATE: 2001-06-29 PRIOR APPLICATION NUMBER: US 08/881,227 PRIOR FILING DATE: 1997-06-24 NUMBER OF SEQ ID NOS: 368 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 186 LENGTH: 273
                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020160456A1el Helicobacter Polypeptides
TITLE OF INVENTION: Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 06132/043002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kleanthous, Harold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191
                                                                     109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 LWAKTKGAF---KYIYDHHLND------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 QNH------DKRAKHVKATWAKRCNKYVFMSSEEDAELPAINLNVS-----
152
                                201 NPALCAGELHYAKFHDONSALGSLIEHDRR 230
                                                                                                         141
                                                                                                                                         49 ALELLEMTGIECVQTIKDKERFKPKDALMEIRGDFSMLLKVERTLLNLLQHSSGIATLTS 108
                                                                                                                                                                                                                                                 41 LERAMAELVPGLSAHPYLSGVEKACFMSHAVLWEQALD---EGVPYIAVFEDDVLLGEGA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 LSGVEKACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSAF 117
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                                                                                                                                                                             EQFLAEDTWLQ----
                                                                                                                                                                                                                 LERALKE----
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DDALMLKDTHLRHVKD----LKSFLTHARK 177
                                                                     REVEALNSHKVRLLDTRKTRPLLRIF-EKYSVLNG-
                                                                                                   RAFPLLESEHCGTAGYIISRKAMRFFLDRFAVLPPERLHPVDLMMFGNPDDREGMPVCQL 200
                                                                                                                                                                                                                                                                                         45; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oomen, Raymond P.
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Tomb, Jean François
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                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                        21.4%;
                                                                                                                                                                             -ERFDP-----DSAFVVRLETMFMHVLTSPSGVADYGG 140
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                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                 ---DLGHGDLFERVLEKDFKATAFVRAKQEGVFSGEKY 48
                                                                                                                                                                                                                                                                                     Score 82.5; Di
Pred. No. 1.9;
33; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----YDWFLKAD------DDTY 190
                                                                                                                                                                                                                                                                                                        .9
                                                                                                                                                                                                                                                                                                                         DB 9;
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                                                                                                                                                                                                                                                                                   73;
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                                                                                                                                                                                                                                                                                                                         Length 273;
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RESULT 7 US-10-235-056-9 ; Sequence 9, Ap

Application US/10235056

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                                                                                                ; TYPE: PRT
; ORGANISM: Synechocystis sp.
US-09-988-626-236
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; ORGANISM: Drosophila melanogaster
US-10-235-056-9
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Best Local Similarity
Matches 44; Conserv
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Query Match 5.5%; Score 81; DB 9; Best Local Similarity 21.5%; Pred. No. 7.1; Matches 64; Conservative 37; Mismatches 9
                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0.
SEQ ID NO 236
LENGTH: 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 236, Application US/09988626 Publication No. US20030044959A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publication No. US20030059915A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/235,056
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: US 09/461,321
PRIOR FILING DATE: 1999-12-15
                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/564,805
PRIOR FILING DATE: 2000-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 25
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TITLE OF INVENTION: CORE 1 3-GALACTOSYL TRANSFERASES
FILE REFERENCE: 5820.630
                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/434,382 PRIOR FILING DATE: 1999-11-05
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/107,468 PRIOR FILING DATE: 1998-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Canfield, William M. APPLICANT: Cummings, Richard D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tavtigian, Sean V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 KRCNILLFMS-----SGADEELPTVKL---DV--GEGRENLWAK---VKEAFKYVYHHH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 GTVVNEDIEIGR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 AMREFIDREAVLPPERLHPVDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQNSAL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 YNDADFFYKADDDTYAVIENMRYMLYPYNPETPVHFGFKFKPFVKQGYMSGGAGYILSRE 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 -----PDSAFVVRLETMFMHVLTSPSGVADYGGRAFPLLESEH-CGTAGYIISRK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 KAC----FMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFD----- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSLIEHDRRLNR 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simard, Jacques
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.6%; Score 82.5; DB 9; Length 366; 22.9%; Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
    99;
                                              Length 554;
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    Indels
    98;
Gaps
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    17;
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| | . Qy | FGSRGIPFQFFDALMPSERLERAMAELVPGLSAHPYLSG |
|---|------------------|---|
| | ğ | YGNRRLPHRRQQEKQFIQA1ETVLAKGRNILLPVPPLGLAQ-EILKLLRTHHQFTGRQVN |
| | Qy | 61YEKACFMSHAYL-WEQALDEGYPYIAYFEDDVLLGE 95 |
| | ర్జ | 250 LWAGESVARGCDAYQGIIDHLPDNVRNFAQHQPLFWD DKVYPHLRPLTDDQGELS 304 |
| | Qy | VRLETMEM-HVLTSPSGVAD |
| | ₽ | 305 LSAPSIVITTTWPAFWPSPAALPGLWTVFMPQLLTLPSCLVNFAWQDLEEEPKYELED 362 |
| | Qy | RLHPVDLMMFGNPDDREGMPVCQL |
| | Db | 363 YLLADHSDGRNTTQLIHNLRPQHLVFVHGQPSDIEDLTSLEELQSRYQLHSP 414 |
| | Qy | HYAKFHDQNSALGSLIEH-DR |
| | Db | 415 AAGNAVALPIGDRFVQPTPPPPQIYEGEIHELEPNKQIHHLGEVVIHLDGQILENSRW 472 |
| | RESU | • |
| | ; Se | 23 |
| | ; ; | 茰 |
| | P P | APPLICANT: Teng, David H.F. |
| | | Simarc |
| | | Myriad Genetics, Inc. |
| | н | ITLE OF INVENTION: CHAOMOSOME 1/p-Hinsed Flostate Cancel Susceptibility |
| | v. | NUMBER: US/09/988,687 |
| | 9 0 | URRENT FILING DATE: 2001-11-20 RIOR APPLICATION NUMBER: 09/564,805 |
| • | יי יי פין פין | PRIOR FILING DATE: 2000-05-05 PRIOR APPLICATION NUMBER: US 60/107,468 |
| • | g g | APPLICATION NUMBER: 09/ |
| | 2 Z T | PRIOR FILING DATE: 1999-11-05 NUMBER OF SEQ ID NOS: 240 SOFTWARE: Datentin Ver 2 0 |
| | ; SEQ | ID NO 236 ENGTH: 554 |
| | ; ; | ORGANISM: Synechocystis sp. 09-988-687-236 |
| | ₩ B Q u | Query Match 5.5%; Score 81; DB 9; Length 554; Best Local Similarity 21.5%; Pred. No. 7.1; Matches 64. Conservative 37. Mismatches 00. Indels 08. Case 17. |
| | Qy | 22 FGSRGIPFQFFDALMPSERLERAMAELVPGLSAHPYLSG 60 |
| | ₽. | 191 YGNRRLPHRRQQEKQFIQAIETYLAKGRNILLPYPPLGLAQ-EILKLLRTHHQFTGRQVN 249 |
| | Qy | QALDEGVPY |
| | ф | 250 LWAGESVARGCDAYQGIIDHLPDNVRNFAQHQPLFWDDKVYPHLRPLTDDQGELS 304 |
| | Qy | M-HVLTSPSGVAD |
| | Db | 305 LSAPSIVITTIWPAFWPSPAALPGLWTVFMPQLLTLPSCLVNFAWQDLEEFPKYELED 362 |
| | Qy | 151 CGTAGYIISRKAMRFFLDRFAVLPPERLHPVDLMMFGNPDDREGMPVCQLN 201 |
| | D b | 363 YLLADHSDGRNTTQLIHNLRPQHLVFVHGQPSDIEDLTSLEELQSRYQLHSP 414 |
| | Qy | 202PALCAQELHYAKFHDQNSALGSLIEH-DRRLNRKQQW 237 |
| | - | HELEPNKOTHHIGEVVIHI.DGOTLENS |

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                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                      OTHER INFORMATION: MAP TO AC005532.1
OTHER INFORMATION: EXPRESSED IN PLACE, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: SWISSPROT HIT: Q50950, EVALUE 4.90e-01
OTHER INFORMATION: EST_HUMAN HIT: BE336820.1, EVALUE 1.00e-112
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
86
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APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 09/608,408
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FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/0066
                                    EGAEQFLAED-----TWLQERFDPDSAFVVRLETMFMHVLTSPSGVADYGGRAF- 143
EDADWFLKADDDTYVILDNLRWLLSKYDPEEPI-
                                                                                                                                                                                                                                                                                                                                                                      222
                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATION NUMBER: PCT/US01/00663
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                                                                                   Conservative
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ON NUMBER: PCT/US01/00662
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                                                                                                   5.5%;
                                                                                                   Score 80;
Pred. No.
                                                                                   Mismatches
                                                                                                     2.6;
                                                                                                                         DB 10; Length 222;
                                                                                   19;
                                                                                 Indels
                                                                                 32;
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                                                            US-10-235-056-11
                                                                             RESULT 12
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GENERAL INFORMATION:
                  Sequence 11, Application US/10235056 Publication No. US20030059915A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 54, Appublication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Scarecrow Gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR ETILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/253,007
CURRENT FILING DATE: 2002-09-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 08/842,445
PRIOR FILING DATE: 1997-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 5914-074-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 08/638,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)...(285)
OTHER INFORMATION: Xa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                         114 --LHHMP-----DESVS-VEKYRDRLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 PYVKQGYMSGGAGYVLSKEALKREVDAF 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 PLLESEH-CGTAGYIISRKAMRFFLDRF 170
                                                                                                                                     253 KLGGHEGALYLFWKRRPMATCSVWKPNP 280
                                                                                                                                                                          220 ALGS-----LIEHDRRLNRKOOWRDSP 241
                                                                                                                                                                                                                 203 ACEESERVERHEVLGKWR---VRMMMAG----FTGWPV-STSAAFAASEM--LKAYDKNY 252
                                                                                                                                                                                                                                                                                                151
                                                                                                                                                                                                                                                                                                                                  125 FMHVLTSP-----SGVADYGGRAFPLLES-----
                                                                                                                                                                                                                                                                                                                                                                                                             65 CFMSHAVLWEQALDEGVPYTAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSAFVVRLETM 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 LSLVGERLATLAQ---SCGVPFEFHDAIMSGCKVQREHLGLEPGFAVVVNFPYV----- 113
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                                                                                                                                                                                                                                                                                            --NTNTSPLVSRFVETLDYYTAMFESIDAARPRDDKQRISAEQHC-----VARDIVNMI 202
                                                                                                                                                                                                                                                     -----LDRFAVLPPERLHPVDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQNS
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Pred. No. 3.6;
35; Mismatches
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16;

APPLICANT: Canfield, William M.
APPLICANT: Cummings, Richard D.
APPLICANT: Ju, Tongzhong
TITLE OF INVENTION: CORE 1 3-GALACTOSYL TRANSFERASES
FILE REFERENCE: 5820.630

CURRENT APPLICATION NUMBER: US/10/235,056
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: US 09/461,321

PRIOR FILING DATE: 1999-12-15 NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn version 3.1

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US-09-849-031A-1
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; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-235-056-11
SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                           Sequence 1, Application US/09849031A Patent No. US20020026033A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
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Best Local Similarity
                                     PRIOR APPLICATION NUMBER: 09/334,013 PRIOR FILING DATE: 1999-06-15 NUMBER OF SEQ ID NOS: 40
                                                                                              CURRENT APPLICATION NUMBER: US/09/849,031A CURRENT FILING DATE: 2001-05-04
                                                                                                                                APPLICANT: Cummings, Richard D.
APPLICANT: McEyer, Rodger P.
TITLE OF INVENTION: synthetic glycosulfopeptides and methods of synthesis thereof
FILE REFERENCE: 5820.593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/235,056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/461,321
PRIOR FILING DATE: 1999-12-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: Cummings, Richard D.
PPLICANT: Ju, Tongzhong
TILE OF INVENTION: CORE 1 3-GALACTOSYL TRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                           144 PLLESEH-CGTAGYIISRKAMRFFLDRF 170
                                                                                                                                                                                                                                                                                                                                                                                                                    160 EDADWFLKADDDTYVILDNLRWLLSKYDPEEPI
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26.1%;
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Pred. No. 4.8;
4; Mismatches 1
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Search completed: May 27, 2003, 18:23:31 Job time: 25 secs

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; TYPE: PRT
; ORGANISM: HOMO Sapiens
US-09-849-562A-1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-031A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
                                                                                                                                              Query Match
Best Local Similarity
Matches 23; Conserv
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Matches 23; Conserv
                                                                                                                                                                                                                                                                                               SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09849562A Patent No. US20020042102A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/849,562A CURRENT FILING DATE: 2001-05-04 PRIOR APPLICATION NUMBER: 09/334,013
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cummings, Richard D. APPLICANT: McEver, Rodger P. TITLE OF INVENTION: synthetic glycosulfopeptides and methods of synthesis thereof FILE REFERENCE: 5820.594
                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-(NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
 200
                                    144 PLLESEH-CGTAGYIISRKAMRFFLDRF 170
                                                                        160 EDADWFLKADDDTYVILDNLRWLLSKYDPEEPI-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 PLLESEH-CGTAGYIISRKAMRFFLDRF 170
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                                                                                                              95 EGAEQFLAED---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 EGAEQFLAED-----TWLQERFDPDSAFVVRLETMFMHVLTSPSGVADYGGRAF- 143
PYVKQGYMSGGAGYVLSKEALKRFVDAF 227
                                                                                                                                              Conservative
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                                                                                                            -----TWLQERFDPDSAFVVRLETMFMHVLTSPSGVADYGGRAF- 143
                                                                                                                                                               5.5%; Score 80; DB 26.1%; Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.5%; Score 80; DB 10; 26.1%; Pred. No. 5.1;
                                                                                                                                                14; Mismatches
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                                                                                                                                                                                 DB 10;
                                                                                                                                                19;
                                                                                                                                                                                   Length 363
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                                                                                                                                              Indels
                                                                        YFGRRFK 199
                                                                                                                                              32;
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Run on:
                                                                             OM protein -
                                                                           protein search,
                                        May 27,
                                                                                                                                 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
2003, 18:12:59; Search time 45 Seconds (without alignments) 596.033 Million cell
                                                                           using sw model
 updates/sec
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Title: Perfect score: US-10-007-267A-8 1461

Sequence: MQNHVISLASAAERRAHIAA... REKRRORREQLIGKTIVPFQ 279

Scoring table: BLOSUM62 Gapop 10.0 ,

Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum Maximum DB DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pir1:*
pir2:*
pir3:*
pir4:*

Database

PIR_73:*

Pred. No. and is No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.

SUMMARIES

| 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | o | ហ | 4 | ω | 2 | 1 | Result No. |
|-----------|--------------------|--------------------|--------------------|--------------------|-------------------|--------|--------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------|--------|----------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------------|
| 88 | 88 | 89.5 | 89.5 | 90 | 90.5 | 90.5 | 91 | 91 | 91 | 93.5 | 93.5 | 95.5 | 99 | 99.5 | 100.5 | 107 | 116.5 | 128 | 231.5 | 271 | 418 | 461 | 881.5 | 928.5 | 997.5 | 1288 | 1293 | 1329 | Score |
| 6.0 | | | | | | | | | 6.2 | | 6.4 | | | | | | | 8.8 | | 18.5 | 28.6 | 31.6 | 60.3 | 63.6 | 68.3 | 88.2 | 88.5 | 91.0 | Query Match |
| 694 | 292 | 1378 | 737 | 284 | 404 | 383 | 735 | 266 | 266 | 1571 | 444 | 419 | 492 | 273 | 267 | 738 | 721 | 332 | 268 | 282 | 302 | 266 | 276 | 280 | 268 | 275 | 275 | 279 | Length |
| ۵ | N | N | ผ | – | N | N | N | ν | N | N | N | N | 2 | Н | N | N | 2 | N | N | N | - | N | N | N | N | N | N | 2 | B |
| B86559 | D71894 | T30173 | C84232 | E64620 | C64597 | T30730 | S76425 | н97576 | AG2797 | T14155 | F71916 | T19837 | T20368 | B64623 | E64175 | T00343 | AH3417 | E71916 | AD3304 | F64091 | A64077 | S71025 | S70815 | A81027 | в81971 | S70814 | C81027 | A81971 | Ħ |
| on factor | probable lipopolys | zinc finger protei | kinase anchor prot | lipopolysaccharide | lipopolysacharide | | | hypothetical prote | conserved hypothet | zinc finger protei | \sim | | hypothetical prote | 7 | | . hypothetical prote | lpsA protein [impo | probable lipopolys | lipooligosaccharid | lipopolysaccharide | lipopolysaccharide | lipopolysaccharide | glycosyl transfera | lacto-N-neotetraos | lacto-N-neotetraos | glycosyl transfera | lacto-N-neotetraos | lacto-N-neotetraos | Description |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | <u>ب</u> ھو | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | |
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| 83.5 | 83.5 | 84.5 | 84.5 | 84.5 | 86 | 86 | 86 | 86 | 86.5 | 86.5 | 87 | . 87 | 87.5 | 87.5 | 88 | |
| 5.7 | 5.7 | 5.8 | 5. 8 | 5.8 | 5.9 | 5.9 | 5.9 | 5.9 | 5.9 | 5.9 | 6.0 | 6.0 | 6.0 | 6.0 | 6.0 | |
| 435 | 402 | 410 | 339 | 339 | 5069 | 361 | 300 | 258 | 845 | 354 | 273 | 256 | 1153 | 404 | 694 | |
| N | N | N | N | N | N | N | N | N | N | N | N | N | N | N | 2 | |
| JN0290 | B34735 | G81596 | G86551 | в72072 | T17464 | C83350 | A97607 | AC2829 | T17291 | S77119 | E71890 | T00097 | A97179 | C71907 | G72065 | |
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Nature 404, 502-506, 2000 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis A;Reference number: A81775; MUID:20222556; PMID:10761919 lacto-N-neotetraose biosynthesis glycosyl transferase NMA0525 [imported] - Neisseria C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83817.1; PID:g737 A;Experimental source: serogroup A, strain Z2491 R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; A; Molecule type: DNA A; Residues: 1-279 < PAR> A; Accession: A81971 A;Status: preliminary Holroyd, S.; Jagels, K.; ture 404, 502-506, 2000 Accession: Genetics S.D.; Churcher, C.; Klee, Mungall, K.; Quail, M.A.; S.R.; Mo Rajandre

A,Gene: lgtB; NMA0525 C;Superfamily: lipopolysaccharide biosynthesis-associated protein

Query Match Matches Local Similarity Conservative 91.0%; 5 Score 1329; DB 2; Pred. No. 6.1e-115; 5; Mismatches 16; Length 279; Indels 0 Gaps 0

밁 Ş 1 MQNHVISLASAAERRAHIAATFGSRGIPFQFFDALMPSERLERAMAELVPGLSAHPYLSG 60 60

밁 ğ 61 VEKACEMSHAVLMKQALDEGLPYIAVFEDDVLLGEGAEKFLAEDAMLQERFDPDSAFIVR 61 VEKACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSAFVVR 120 120

Ş 121 LETMFMHYLTSPSGYADYGGRAFPLLESEHCGTAGYIISRKAMRFFLDRFAVLPPERLHP 180

ğ 181 VDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRRLNRKQQWRDS

LETMFMHVLTSPSGVADYCGRAFPLLESEHWGTAGYIISRKAMWFFLDRFAALPSEGLHP

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밁 181 VDWMMFGNPDDRERMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRCLNSKQQRRDS

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RESULT C81027

lacto-N-neotetraose biosynthesis glycosyl transferase LgtB NMB1928 [imported]
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: C81027 Neiss

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Hickey, E.K.;
ri, H.; Qin, I
Science 287,
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A;Title: Molecular analysis of a locus for the biosynthesis an A;Reference number: S70812; MUID:96414473; PMID:8817494
A;Accession: S70814
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A;Nolecule type: DNA
A;Residues: 1-275 <TET>
A;Cross-references: GB:AE002541;
A;Cross-imental source: serogroup
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C; Genetics:
A; Gene: NMB1928
C; Superfamily: lipopoly
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;Species: Neisseria meningitidis
;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_cha
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7; Mismatches 17;
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ri, H.; Qin, H.; Vamathevan, J.; Gill, Science 287, 1809-1815, 2000
A; Authors: Grandi, G.; Sun, L.; Smith,

; Vamathevan, J.; 809-1815, 2000

A; Title: Complete A; Reference number

genome

sequence of Neisseria 00; MUID:20175755; PMII

H.O.; Fraser, C.M.; Moxon,

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R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; ri, H.; Qin, H.; Vanathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.;

lacto-N-neotetraose biosynthesis glycosyl transferase LgtE NMB1926 [imported] C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: A81027

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A; Gene:
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A;Title: Complete DNA sequence of a serogroup A strain of A:Reference number: A81775; MUID:20222556; PMID:10761919
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C;Accession: B81971
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                                                                                                                                                                                                                                                                                                                        68.3%; Score 997.5; 72.9%; Pred. No. 2.30 Live 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:AL157959; NID:g7379120; A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K.D.;
S.; Mc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moule,
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                                                                                                                                                                                                                                                                                                                                     2.3e-84;
                                                            -OSETLPSQLKNGRQESYRN--RRS
                                                                                                                                                                                                                                                                                                                                                        DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.D.; Churcher, C.;
Mungall, K.; Quail,
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                                                                                                                                                                                                                                                                                                                                                    Length 268;
                                                                                                                                                                                                                                                                                                                                                                                      protein
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M.A.;
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Rajandre
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RESULT 6
$7/815
$1/900$7 transferase E (EC 2.4.-.-) - Neisseria meningitidis
$1/900$7 transferase E (EC 2.4.-.-) - Neisseria meningitidis
$1/900$7 (Species: Neisseria meningitidis
$1/900$7 (C.) Accession: $7/915
$1/900$7 (Species: S7/915)
$1/900$7 (Species: SPecies: SPecie
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-280 <TET>
A;Cross-references: GB:AE002541;
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A;Title: Molecular analysis of a locus for the biosynthesis au A;Reference number: S70812; MUID:96414473; PMID:8817494
A;Accession: S70815
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A; Residues: 1-276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Cross-references: EMBL:U25839; NID:g973183;
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VDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDRRLNRKQQWRDS
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                                                                               LETMFAKVIVRPDKVLNYENRSFPLLESEHWGTAGYIISREAMRFFLERFAVLPARVDKA
                                                                                                                                                                                          VEKACFMSHAVLWKQALDEGLPYVAVFE---
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 881.5;
Pred. No. 1.2e
?7; Mismatches
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Pred. No. 5.6e
Pred. No. 5.6e
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Geoghagen,

Weidman, N.S.M.

Kerlavage

influenzae

A64077

A; Reference number: A; Accession: A64077

A; Molecule type: DNA A; Residues: 1-302 <TIGR> A;Status: nucleic acid sequence

A; Experimental R; Cope, L.D.; Y

Yogev, source:

strain Rd KW20.; Mertsola, J.

A;Cross-references: GB:U32736; GB:L42023; NID:g1573519; PIDN:AAC22208.1; PID:g1573535

Latimer,

J.L.;

M.S.;

a

not shown;

translation not

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R;High, N.J.; Jennings, M.P.; Moxon, E.R.
Mol. Microbiol. 20, 165-174, 1996
A;Title: Tandem repeats of the tetramer 5'-CAAT-3' present
A;Reference number: S71024; MUID:97014379; PMID:8861214
A;Recession: S71025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; High, N.J.; Jenni
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A; Residues: 1-266 <HIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental
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                                                                                                                                                                                  KACFMSHYMLWQKCFSEDLPYIYIFEDDVLLGENADKFLAEDEWLEEAFKQTDKFILRFE
                                                                                                                                                                                                  KACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSAFVVRLE
                                                                                                                                                                                                                                             NYVISLTSAYQRREHIQKEFSQQNIPFEFFDALKPSKELTSLIEKFIPNL-LHAKLTEGE
--RTLKTVLISLAGK--PKKILRKIYRKLFISKHIVPFR
                           PANTFKHRLIRALTKIGREREKRRORREQLIGKIIVPFQ
                                                            LLMF - - - -
                                                                                                                      TFLNFSKCKDKKIKPYSGRKILKLVSENCGAAGYVISREAVKOLSAHICSLTSNHLLAID
                                                                                                                                        VDWMMFTYFFDKEGMPVYQVNPALCTQELHYAKFLSKNSMLGSDLEKDREQER---
                                                                                                                                                                                                                                                                                                            109;
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                                                                                                                                                                                                                                                                                                                                                                    required for the biosynthesis of a phase-variable lipopolysaccharide biosynthesis-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                    source:
                                                           ·NIFNQSTYQVSPGVCVQE----GQLYPKDIKLHSQLETERQKYLSVKKK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: 254182; NID: g1150402; ce: strain RM7004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #sequence_revision 13-Mar-1997
                                                                                                                                                                                                                                                                                                                         31.6%;
39.1%;
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                                                                                                                                                                                                                                                                                                                       Score 461; DB 2;
Pred. No. 7.2e-35;
                                                                                                                                                                                                                                                                                                          Mismatches
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A; Residu
A; Cross-
C; Geneti
A; Start
                                                                                                                                        C;Accession: F64091

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlayage, ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, , D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
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A; Note: it is uncertain whether Met-1 or Met-11 is the initiato: R; High, N.J.; Deadman, M.E.; Moxon, E.R.
Mol. Microbiol. 9, 1275-1282, 1993
                                                                                                                                                                                                                                                                                                                                      lipopolysaccharide biosynthesis protein lic2B homolog - Haemophilus influen C;Species: Haemophilus influenzae C;Date: 18 -Aug-1995 #sequence_revision 18 -Aug-1995 #text_change 20 -Sep-1999 C;Accession: F64091
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A;Title: The role of a repetitive DNA motif
A;Reference number: S39576; MUID:95020659; P
A;Accession: S39576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Microbiol. 5, 1113-1124, 1991
A; Title: Molecular cloning of a gene involved in lipooligosaccharide biosynthesis
A; Reference number: S15282; MUID:92065807; PMID:1956289
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;Residues: 1-28,'N',30-40,49-105,'L',107-150,'R',152-255,'P',257-273,'D',275-302
;Cross-references: EMBL:L19441; NID:g305379; PIDN:AAA65534.1; PID:g305380
;Experimental source: strain RM7004
                                                 Cross-references:
                                                                        Residues:
                                                                                                                  Status: nucleic acid sequence not shown; translation not shown
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                                                                                            Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVPF 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISRKAMRFFLDRFAVLPPERLHPVDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NQSINQSNSILHNIEESRILTKGEKGCLISHFLLWNKCVNENFEYLKIFEDDVILGENAE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERAMAE ----LVPGLSAHPYLSGVEKACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAE
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                                                                        <TIGR>
                                               GB:U32760;
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                                               GB:L42023; NID:g1573764;
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Pred. No. 7
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PMID:7523834
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                                               PIDN: AAC22423.1;
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                                            PID:g1573773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE008917; PIDN:AAL51599.1; A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: AD3304

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.;

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative

A;Reference number: AD3252; PMID:11756688

A;Accession: AD3304
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A; Residues: 1-268 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lipooligosaccharide biosynthesis protein lic2B [imported] -
;Species: Brucella melitensis
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
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211
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                                                                                                                                                              104 DTWLQERFDPDSAFVVRLETMFMHVLTSPSGVADYGGRAFPLLESEHCGTAGYIISRKAM 163
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                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                    -----VPGLSAHPYLSGVEKACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAE
                                                                                                                                                                                                                                                                MKCYLINLDKSRDRLEFMASQFERLGAQF-----ERVEAVNGRAMSPLELASFTQI
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                             GSLIEHDRRLNRKQQ-----
                                                              RKLLP----LMEKVSAPVDHFLF-DPNDGPFNDFEIYQISPAICRQ-----
                                                                                              RFFLDRFAVLPPERLHPVDLMMFGNPDDR--EGMPVCQLNPALCAQELHYAKFHDQNSAL
                                                                                                                               DHWI-----PKQADIVKIDAYGHEVLIS-NPVKNEGPYSISRLRSRHLQTGGYVVSREAA 166
                                                                                                                                                                                               SKEWPAP-----LSPAEIGCFLSHRKCLEKIAAGEDAYAAVFEDDIRLSQGSSRFLAS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --PDNPFESSL----QEGRDRVHGNQRKSSILEKI 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSPANTFKHRLIRALTKIGREREKRRQRREQLIGKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LETMFMHVLTSPSGVADYGGRAFPLLESEHCGTAGYIISRKAMRFFLDRFAVLPPERLHP 180
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                                                                                                                                                                                                                                                                                                                                                 15.8%;
28.6%;
                          WRDSPANTFKHR-----LIRALTKIGR
                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43:
                                                                                                                                                                                                                                                                                                                                Score 231.5; DB 2;
Pred. No. 1.1e-13;
3; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 271; DB 2;
Pred. No. 2.6e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Patra, G.; Mu
P.H.; Hagius,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intracellular pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PID:g17982323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , G.; Mujer,
Hagius, S.; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                  Indels
257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brucella melitensis
                                                                                                                                                                                                                                                                                                                                  67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSPDB:GN00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O'Callaghan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.; Los,
                                                              SGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                Gaps
                                                              210
                                                                                              221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brucella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₽.;
                                                                                                                                                                                                                                                                                                                                  12;
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D.; Let
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lpsA protein [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AH3417
R;Dellvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R;Dellvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R;Dellvecchio, V.G.; E, Selvec, P.H.; Hagius, S.; O'Callaghan, D.; Letess Mazur, M.; Goltsman, E.; Selvec, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
                                                                 A; Gene
A; Map
                                                                                                          A;Cross-references: GB:AE008917; PIDN:AAL52507.1; A;Experimental source: strain 16M C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
AH3417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE001489; GB:AE001439; NID:g4155102; PIDN:AAD06135.1; A;Experimental source: strain J99 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682 A;Accession: E71916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999 (c;Accession: E71916 R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; I Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Nature 397, 176-180, 1999
                                                                                                                                                                                                                                           A; Reference number: AD3252; A; Accession: AH3417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable lipopolysaccharide biosynthesis protein - Helicobacter pylori (strain J99)
C; Species: Helicobacter pylori
A; Variety: strain J99
                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-721 <KUR>
                                                                                                                                                                                                                    A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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                                                                                        Gene: BMEI1326
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                                                                   position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149
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  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLDQP-VVILEDDVTLESHFMQAL-EDC-LKSPFD-----FVRLYGCYWYYHETKF-HVL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOIFDAISPKHODFEKLLGELYNAQSLLQSDWYHSYVGAGLTLPELGCYLSHYLLWKECV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFFLEHFYLTSVYVASTAGYYLTPKGAKTFIE--ATESFKIIEPVDMFM----DNSAYHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOFFDALMPSER-LERAMAELVPGLSA-----HPY----LSGVEKACFMSHAVLWEQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GREREKRRORREQLIGKIIVPFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VCQLNPALCAQELHYAKFHDQNSALGSLIEHDRRLNRKQQWRDSPANTFKHRLIRALTKI 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSPSGVA----DYGGRAFPLLES-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSAFVVRL-----ETMFMHVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---NAKKRLNAFQQYSKQYAPLK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --PREFVFPPFDHSFKNNPILEKFKKFFDVSRFLNLSTHKVIHYILKKIQKSYYATHEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-332 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.8%;
23.8%;
25.8
                                                                                                                                                                                                                                                               PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SEHSLDSTIQKPQKKSLKSYPLPPQKSTFKNLFYYSL---
  . 03;
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  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 128; DB 2;
Pred. No. 0.00051;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
116.5; DB
No. 0.016;
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                                                                                                                                                     PID:g17983318;
                    2;
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                    Length
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                                                                                                                                                     GSPDB:GN00190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yovis, G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
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g.
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A;Title: Prediction of the coding sequences of unidentified human A;Reference number: 214086; MUID:98290545; PMID:9628581
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T00343
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                                                                                                                                                                                                                                                                                                           A; Note: KIAA0584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein KIAA0584 - human (fragment) C; Species: Homo sapiens (man) C; Date: 01-Feb-199 #sequence_revision 01-Feb-19
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                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AB011156; NID:g3043691; PIDN:BAA25510.1; PID:g3043692
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.;
                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-738 <NAG>
                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: T00343
                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                             Query Match
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627
                              174
                                                         577 LIYIGRKRMQVKEPEKAVPNVAN
                                                                                                                   518 LTRG-EIGCFLSHYSVWKEVIDRELEKTLVIEDDVRFEHQFKKKLMKLMDNIDQAQLDWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 DPDSAFVVRL----ETMFMHVLTSPSGVADYGGRAFPLLESEHCGTAGYIISRKAMRFFL 167
                                                                                                                                                                                458 MINLKRRKDRRDRMLRTLYEQEIEVKIVEAVDGKALNTSQLKALNIEMLPGYRDPYSSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 SALSTM
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                                                                                                                                      Local
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                                                                                                                                                                                                             5 VISLASAAERRAHIAATFGSRGIPFQFFDAL----MPSERLERAMAELVPG----LSAHP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G
                         PPERLHPVD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D-----VVKLVNHRSPLFMSLLETDAG--DRIGRA---IHGPQGSAAAYLVSREGARKLL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VISLASAAERRAHIAATFGSRGIPFQF--FDALMPSERLERA--
                                                                                      SAFVVRLETMFMHVLTSPSGVADYGGRAFPLLESEHC-GTAGYIISRKAMRFFLDRFAVL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSAHPYLSGVEKACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VINMASQPAAYKTVAASIEAYGQGFQLHRIDAVNGHTATQRIGIDDARFDAINGREMLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                              Similarity 23.3
44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---EYGCYRSHSKALESFLSDGSPYGLILEDDVVFTETTSARIHDIIKSLPDF
                                                                                                                                                                                                                                                             7.3%;
                                                                                                                                                                                                                                              40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                                                                             Score 107; DB Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                  from
                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                GB/EMBL/DDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-Feb-1999
                                                           -LVEADYSYWTLGYVISLEGAQKLV---GAN
                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                              83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #text_change
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                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                             22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37;
                                                                                                                                                                                                                                                                                                                                                                                                                                             genes.
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                                                                                                                                                                                                                                           Gaps
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                                                         626
                                                                                                                                                                                 517
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                                                                                                                     576
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R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Ker Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; W. D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: E64175

Kerlavage 1.; Weidman Jen, N.S.M.

Vente Rd. hypothetical protein HI1697 (lsg locus) - Haemophilus influenzae C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999 C;Accession: E64175; S27580

RESULT E64175

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B64623
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A; Experimental source: strain Rd KW20
R; MCLaughlin, R.; Abu Kwaik, Y.; Young, R.; Spinola, S.; Apicella, M.
submitted to the EMBL Data Library, June 1992
A; Description: Characterization and sequence of the lsg locus from Haemophilus influenze
A; Reference number: $27577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKerson, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
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A;Residues: 11-26,'K',28-39,'I',41-55,'S',57-111,'L',113-136,'N',138-139,'N',141-143,
A;Cross-references: EMBL:M94855; NID:g148931; PIDN:AAA24981.1; PID:g148935
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: B64623
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7;Species: Helicobacter pylori
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Start codon:
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Best Local
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es 58; Conserv
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                          -----ACFMSHAVLWEQALDEGVPYIAVFEDDVLLGEGAEQFLAEDTWLQERFDPDSAF 117
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MSLGELGCYASHYSLWEKCIELN-EAICILEDDITLKEDFKEGL---DFLEKHI--QELG 149
                                                                                         QIFDAIY-SKTFEGGLHPLVK-KHLHPYFITQNIKDMGITTNLISEVSKFYYALKYHAKF 95
                                                                                                                                       QFFDALMPSERLERAMAELVPGLSAHPY------LSGVEK------
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                                                                                                                                                                                                           Score 99.5; DB 1; Length 273; Pred. No. 0.17;
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Pred. No. 0.13;
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CRT3_ARATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
NCBI_TaxID=485;
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Q50947;
                                                                                                                                                                                                    InterPro; IPR002654; GT_25.

Pfam; PF01755; Glyco_transf_25; 1.

Lipopolysaccharide biosynthesis; Transferase; Glycosyltransferase.

SEQUENCE 279 AA; 31776 MW; C2219D1A6119D622 CRC64;
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                                                                                                                                                                                                                                                    EMBL; U14554; AAA68010.1;
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- i- PATHWAY: BIOSYNTHESIS OF THE TERMINAL LACTO-N-NEOTETRAOSE
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Exp. Med. 180:2181-2190(1994).

- FUNCTION: ADDS THE SECOND GALACTOSE TO T
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Mismatches 0;
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Best Loc
Matches
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MEDLINE-2022556; PUBMed-10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd

Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehead S., Spratt B.G., Barrell B.G.;

"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGTB_NEIMA
P57033;
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Pfam; PF01755; Glyco_transf_25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              meningitidis Z2491.";
Nature 404:502-506(2000).
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Bacteria; Proteobacteria; beta sul
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16-OCT-2001 (Rel. 40,
15-JUN-2002 (Rel. 41,
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5; Mismatches
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    Transferase; Glycosyltransferase;

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Matches 253
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EMBL; AE002541;
TIGR; NMB1928;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96414473; PubMed-8817494;
Jennings M.P., Hood D., Peak I.R.A., Virji M., Moxon E.R.;
Jennings M.P., Hood D., Peak I.R.A., Virji M., Moxon E.R.;
Molecular analysis of a locus for the biosynthesis and phase-variable
expression of the lacto-N-neotetraose terminal lipopolysaccharide
structure in Neisseria meningitidis.";
Mol. Microbiol. 18:729-740(1995).
                                                                            Lipopolysaccharide biosynthesis; Complete proteome.
CONFLICT 97 97 A ->
                                                                                                                             InterPro; IPR002654; GT_25.
Pfam; PF01755; Glyco_transf_25;
                                                                                                                                                                                                                   use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fcentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                          Science 287:1809-1815(2000).
-I- FUNCTION: ADDS THE SECOND GALACTOSE
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MEDLINE-20175755; PubMed-10710307;
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Bacteria; Proteobacteria;
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AE002541; AAF42257.
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    Transferase; Glycosyltransferase;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002654; GT_25.

Pfam; PF01755; Glyco_transf_25; 1.

Lipopolysaccharide biosynthesis; Transferase; Glycosyltransferase.

SEQUENCE 280 AA; 32420 NW; F043597BA3044407 CRC64;
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35, Last sequence update)
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se biosynthesis glycosyl transferase
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Pred. No. 1.3e
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC STRAIN-MC58 / Serogroup B;

RC STRAIN-MC58 / Serogroup B;

RX MEDLINE-20175755; PubMed-10710307;

RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.L.,

RA Tettelin H., Saunders N.J., Heod D.W., Peden J.F., Dodson R.J.,

RA Elsen J.A., Ketchum K.A., Hood D.W., Pederson J.D., Hickey E.K.,

RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

RA Mason T., Clecko A., Parksey D.S., Blair E., Clittone H., Clark E.B.,

RA Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

RA Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

The strain Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
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                               CONFLICT
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Jennings M.P., Hood D., Peak I.R.A., Virji M., Moxon E.R.;
Jennings M.P., Hood D., Peak I.R.A., Virji M., Moxon E.R.;
Molecular analysis of a locus for the biosynthesis and phase-variable expression of the lacto-N-neotetraose terminal lipopolysaccharide structure in Neisseria meningitidis.";
Mol. Microbiol. 18:729-740(1995).
                                                                                                        Pfam;
                                                                                                                                         TIGR;
                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                             CONFLICT
                                                                        Lipopolysaccharide biosynthesis; Complete proteome.
                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinfo
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                - I - PATHWAY: BIOSYNTHESIS OF THE TERMINAL LACTO-N-NEOTETRAOSE
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STRAIN-MC58 / Serogroup B;
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Bacteria; Proteobacteria; beta subdivision;
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LGTE OR NMB1926.
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                                                                                                                          InterPro;
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                                                                                                         Pro; IPR002654; GT_25.
PF01755; Glyco_transf_25;
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                                                                                                                                                                        U25839; AAC44086.1;
                                                                                                                                                        AE002541; AAF42255.1;
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Best Local
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: INVOLVED IN EXTRACELIULAR LIPOOLIGOSACCHARIDES (LOS)
BIOSYNTHESIS AND VIRULENCE EXPRESSION. INVOLVED IN THE SYNTHES
OF THE OLIGOSACCHARIDE MOIETY OF THE LOS MOLECULE BY ADDING GA
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STRAIN-RM 7004 / S
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15-JUN-2002
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Pfam; PF01755; Glyco_transf_25; 1.
Transferase; Glycosyltransferase; Virulence.
SEQUENCE 266 AA; 31131 MW; 0C68AE9BA249E
                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agréement (S or send an email to license@isb-sib.ch).
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46; Mismatches 106
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01-NOV-1995 (Rel. 32, C
01-NOV-1995 (Rel. 32, I
15-JUN-2002 (Rel. 41, I
 between
the Euro
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                                                          alpha Gal(1-4)beta Gal.";

MOI. MICTODIOI. 9:1275-1282(1993).

MOI. MICTODIOI. 100CVUED IN EXTRACELLULAR LIPOOLIGOSACCHARIDES
-I- FUNCTION: INVOLVED IN EXTRACELLULAR LIPOOLIGOSACCHARIDES
BIOSYNTHESIS AND VIRULENCE EXPRESSION. INVOLVED IN THE SY
OF THE OLIGOSACCHARIDE MOIETY OF THE LOS MOLECULE BY ADDI
-I- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 25-
-I- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-11 IS THE 1
                                                                                                                                                                   STRAIN=RM 7004 / Serotype B;
MEDLINE=95020659; PubMed=7523834;
High N.J., Deadman M.E., Moxon E.R.;
"The role of a repetitive DNA motif (5'-CAAT-3') in the variexpression of the Haemophilus influenzae lipopolysaccharide
                                                                                                                                                                                                                                                                                                               Cope L.D., Yogev R., Mertsola J., Lat:
McCracken G.H. Jr., Hansen E.J.;
"Molecular cloning of a gene involved biosynthesis and virulence expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAEIN
                               This
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LEX1 OR LIC2A OR HI0550.
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MEDLINE=92065807; PubMed=1956289;
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              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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Swiss Institute
Bioinformatics 1
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FEMS
[2]
                         SEQUENCE FROM N.A.
STRAIN-Serotype A1;
MEDIJINE-95301198; PubMed-7781993;
MEDIJINE-95301198; PubMed-7781993;
Potter M.D., Lo R.Y.C.;
"Cloning and characterization of a gene from Pasteurella ni Involved in lipopolysaccharide biosynthesis.";
FEMS Microbiol. Lett. 129:75-81(1995).
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Bacteria; Proteobacteria;
Mannheimia.
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15-JUN-2002
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(Rel. 33, Last sequence (Rel. 41, Last annument)
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63; Mismatches
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness Fleischmann R.D., Adams M.D., Tomb J.-F., Dougherty B.A., Merrick Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
                                                                                                                                                                                                                                   Q57125; O05033;
01-NOV-1997 (Re
01-NOV-1997 (Re
15-JUN-2002 (Re
                                                                                                                                                       Haemophilus
Bacteria; Pr
Haemophilus.
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Pfam; PF01755; Glyco_transf_25; 1.

Lipopolysaccharide biosynthesis; Transferase; SEQUENCE 263 AA; 30871 MW; B07C39ECIDA603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91358346; PubMed=1885539;
Abdullah K.M., Lo R.Y.C., Mellors A.;
"Cloning, nucleotide sequence, and expression
                                                                                                                                                                                                       Hypothetical HI0765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haemolytica A1 glycoprotease gene.";
J. Bacteriol. 173:5597-5603(1991).
-!- FUNCTION: INVOLVED IN THE BIOSYNTHESIS
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93; Conserv
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                                                                                                                                                                       Proteobacteria;
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                                                                                                                                                                      LSG4_HAEIN STAN
P71398; Q48213;
30-MAY-2000 (Rel. 3
30-MAY-2000 (Rel. 3
15-JUN-2002 (Rel. 4
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Hypothetical protein; Transferase; Glycosyltransferase;
Complete proteome.
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Stelence 269:496-512(1995).
STMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 25.
                                                        McLaughlin R.,
                                                                   STRAIN=A2
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SEQUENCE
                       Submitted
                                  "Characterization and influenzae.";
                                                                             SEQUENCE FROM N.A.
                                                                                                    NCBI_TaxID=727;
                                                                                                                 Haemophilus
                                                                                                                           Bacteria; Proteobacteria;
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Hanna M.C., Nguyen D.T., Saudek D.M.,
                                                       Abu Kwaik Y.,
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                      EMBL/GenBank/DDBJ databases
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Pred. No.
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3; Mismatches
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                                                                                                                        subdivision; Pasteurellaceae;
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V., Fraser C.M., Sm
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lsg locus
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., Brandon R.C.
N.S.M.,
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MEDILINE=9535030; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Mexrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.;
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Pfam; PF01755; Glyco_transf
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MEDLINE-20150255; PubMed-10684935;
MEDLINE-20150255; PubMed-10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelbe Read T.D., Brunham R.C., Peterson J., Utterback T., Be: White O., Hickey E.K., Peterson J., Utterback T., Be: Linher K., Weidman J., Khouri H., Craven B., Bowman C., Weidman J., McClarty M., Nelson W., DeBoy R., Kolonay J., McClarty
                   NP_BIND
NP_BIND
                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                              FUSA OR CPN0550 OR CP0202.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                               TIGRFAMS;
                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequences of Chlamydia trachomatis pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99206606; PubMed=10192388;
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
                                                           Elongation
                                                                     PROSITE;
                                                                                         TIGRFAMS;
                                                                                                  PRINTS; PR00315;
                                                                                                                                                  InterPro;
                                                                                                                                                                                         TIGR;
                                                                                                                                                                                                  PHCI-2DPAGE; Q9Z802; -.
                                                                                                                                                                                                             HSSP;
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                                                                                                                                                                     InterPro;
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                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                          EF-G/EF-2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genet. 21:385-389(1999).
                                                                                                                                                                                                                     AE002181;
AP002547;
                                                                                                                                                                                         CP0202;
                                                                                                                                                                                                             P13551; 1DAR
                                                                                                                                                                                                                                          AE001639;
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                                                                                                                                        IPR000640;
IPR004161;
IPR000795;
IPR005225;
                                                                                                                                                                                                                                                                                                           the Swiss Institute of Bioinformatics and the
                                                                     PS00301;
                                                                                                                                                                                                                                                                      requires a license agreement
                                                                                                                                                                                                                                                                                          non-profit
                                                                              TIGR00231; small_GTP; 1.
TIGR00484; EF-G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nelson W., DeBoy
Fraser C.M.;
                                                                                                                                                                              IPR004540;
                                                                                                                                                                                                                                                            email to license@isb-sib.ch).
                                                          factor;
                    18
82
136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Res. 28:1397-1406(2000).
                                                                                                                     GTP_EFTU; 1.
EFG_C; 1.
                                                                                                GTP_EFTU_D2; 1.
5; ELONGATNFCT.
  8
                                                                                                                                                                                                                    AAD18690.1;
AAF38074.1;
BAA98756.1;
                                                                    EFACTOR_GTP; 1.
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86
139
                                                           Protein
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EF_GTPbind.
Small_GTP.
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TO THE GTP-BINDING
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                                                         biosynthesis;
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          P (BY SIMILARITY).
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                                                         GTP-binding;
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Salzberg S.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Okumura S., Shimpo S., Takeuchi C.,
Vamada M., Yasuda M., Tabata S.;
Yamada M., Yasuda M., Tabata S.;
Yamada M., Yasuda M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
DNA Res. 3:109-136(1996).

DNA Res. 3:109-136(1996).
                                                                                                                                                                   entities
or send a
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01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                  + D-alanyl-D-alanine.
- I- PATHWAY: ALONG WITH ALANINE RACEMASE, IT MAKES UP THE D-ALANINE RACEMASE, IT MAKES UP THE D-ALANINE BRANCH OF THE PEPTIDOGLYCAN BIOSYNTHETIC ROUTE (BY SIMILARITY)
- I- SUBCELLULAR LOCATION: Cytoplasmic (By Similarity).
- I- SIMILARITY: BELONGS TO THE D-ALANINE-D-ALANINE LIGASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nak
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.
Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ul-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
D-alanine--D-alanine ligase (EC 6.3.2.4) (D-alanylalanine synthetase)
(D-Ala-D-Ala ligase).
                   InterPro; IPR000291; Dala_Dala_ligase Pfam; PF01820; Dala_Dala_ligas; 1. TIGREAMS; TIGR01205; D_ala_D_alaTIGR;
                                                                                                   EMBL; D90908; BAA17677.1;
HSSP; P07862; 1IOV.
                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced throubetween the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synechocystis sp. (strai
Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97061201; PubMed-8905231;
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                                                                                                                                                                              s requires a license agreement (san email to license@isb-sib.ch).
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Matches 43
                                                                                             EMBL;
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Submitted (NOV-1996) to
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                                                                                                                                                                                                                                                                                                                                                         Nature New Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                 Morrison T.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=71240788; PubMed=5283385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION
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                                                                                                                                                                                                                                                                                                                    FUNCTION: RESPONSIBLE FOR GROWTH OF BACTERIOPHAGE
                                                                                                                                                                                                                         European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                             translational
                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                    CARRIES THE PLASMID
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Peptidoglycan synthesis; Comp., 38774 MW; 871B82362A47315A
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741
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DQVSPFFDDWPAVEEKLKVMLSGNELTPEQEALKTALENDD
-> VTRSVRSLMTGQQSKRS (IN REF. 2).
; 4C373DF929AFCD65 CRC64;
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Best Local S
Matches 75
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=90367113; P Ghosh S., Gifford A Baltimore D.;
                          carboxyl terminic
protein kinase A.";
protein kinase A.";
                                                                                                                                                                                                                                                                                                                                                  Ol-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nuclear factor NF-kappa-B p105 subunit (DNA-binding factor KBF1) (EBP-
1) (NF-kappa-B1 p84/NF-kappa-B1 p98) [Contains: Nuclear factor NF-
kappa-B p50 subunit].
                                                                                                                             Grumont R.J., Fecondo J., Gerondakis S.;
"Alternate RNA splicing of murine nfkbl generates a n of the p50 precursor NF-kappa Bl that can function as transactivator of NF-kappa B-regulated transcription. Mol. Cell. Biol. 14:8460-8470(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                              KBF1_MOI
P25799;
                                                                                      Gerondakis
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
 MEDLINE=92191289;
            SEQUENCE
                                                                                                            SEQUENCE
                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS P84 MEDLINE=95059075; PubMed=7969179;
                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                               "The activity of a 70
                                                                                               MEDLINE=94001687;
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                          "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239
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                                                                                                                                                                                                                      62:1019-1029(1990).
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            365-971
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hara; Chordata;
                                                                                      Morrice
                                                                                                                                                                                                                                        p50 DNA binding
                                                     of.
                                                                                              71 FROM N.A., AN PubMed=8398903;
                                                                                                                                                                                                                                                                 A.M.,
71 FROM N.A.
PubMed=1339305;
                                                                                                                                                                                                                                                                          PubMed=2203532;
            FROM
                               4:617-627(1993)
                                                                                                                                                                                                                                                                                                                    Rodentia;
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22.1%;
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the p105 NF-kappa
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                                                                                                                                                                                                                                                                Riviere
                                                                                      Richardson
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Pred. No. 6.9;
80; Mismatches
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-kappa B
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                                                                                                                                                                                                                                                                G.P.,
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-!- FUN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   x-ray Crystallography (2.9 angstroms) of MEDLINE=98111237; PubMed=9450761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huxford T., Huang D.B., Malek S., Ghosh G.; "The Crystal structure of the KappaBalpha/NF-kappaB complex reveals mechanisms of NF-kappaB inactivation."; Cell 95:759-770(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MEDLINE=99081292; PubMed=9865694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            crystal structures of the dimerization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MEDLINE=98046092; PubMed=9384558; Huang D.B., Huxford T., Chen Y.Q., Ghosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ghosh G., van Duyne.G., Ghosh S., Sigler P.B. "Structure of NF-kappa B p50 homodimer bound Nature 373:303-310(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMEDLINE=95132005; PubMed=7530332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lin L., DeMartino G.N., Gree "Cotranslational biogenesis Cell 92:819-828(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9529257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huang D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99081292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The role of DNA in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
after the GRR repeat may promote the generation of p50 mak an acceptable substrate for the proteasome. The processed active and the unprocessed form acts as an inhibitor (I kalike), being able to form cytosolic complexes with NF-kapp trapping it in the cytoplasm. Complete folding of the region downstream of the GRR repeat precludes processing. PTM: Polyubiquitination seems to allow P105 processing. SIMILARITY: BELONGS TO THE REL/DORSAL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Nuclear, but also found in an inactive form complexed to an inhibitor ALTERNATIVE PRODUCTS: 3 isoforms; pl05 (shown
                                                                                                                                                                                                                          DOMAIN: Glycine-rich region (GRR) in the generation of p50.
PTM: While translation occurs, the
                                                                                                                                                                                                                                                                                                                        are produced by alternative splicing INDUCTION: By phorbol ester and TNF-alpha. DOMAIN: The C-terminus of p105 might be involved in cytoretention, inhibition of DNA-binding, and transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Play a role in the regulation of apoptosis.
FUNCTION: NF-kappa-B p98 subunit (but not p84 or p105) a transactivator of NF-kappa B-regulated gene expression.
SUBUNIT: Active NF-kappa-B is a heterodimer of an about
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of genes involved in immune response and acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a cotranslational processing. The proteasome-mediated process ensures the production of both p50 and p105 and preserves their independent function, although processing of NPKBI/p105 also appears to occur posttranslationally. p50 binds to the kappa-B consensus sequence 5'-GGRNNYYCC-3', located in the enhancer region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Appears to have dual functions retention of attached NF-kappaB proteins a cotranslational processing. The proteas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-binding subunit and the heterodimers might form a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  appa B gamma, a 70 kd protein identical to the C-terminal half NF-kappa B: a new member of the I kappa B family."; 68:1109-1120(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391:410-413(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the mechanism of NFkappaB dimer formation:
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esis of NF-kappaB p50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the weak DNA-binding subunit p65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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; 1NFK; 23
; 1BFS; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1BFT;
1VKX;
1IKN;
 GVEKACFMSHAVLWEQA-LDEGV-
                                     ISLAGCLLLEGDAHVDST
                                                                    ISLASA - - AERRAHIAATFGSRGIPFQFFDALMP - - - - SERLERAMAELVPGLSAHPYLS
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S66656; AAB28573.1;
S89033; AAB21851.1;
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TESLTGDSPLLSLNKMPHGYGQEGPIEGKI -> MNSGIVT
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
               Mulligan L.M., Kwok J.B.J., Healey C.S., Elsdon M.J Gardner E., Love D.R., Mole S.E., Moore J.K., Papi Telenius H., Tunnacliffe A., Ponder B.A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proto-oncogene (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P07949;
01-AUG-1988
                                                                                                                                                                                               VARIANTS MEN2A/MTC W-611; S-618; MEDLINE-93372843; PubMed-8103403;
                                                                                                                                                                                                                                                 hirschsprung disease.";
Hum. Mutat. 9:97-109(1997).
                                                                                                                                                                                                                                                                                neoplasia type 2 syndromes,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Hofstra R.M.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-87257826;
Takahashi M., Coop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 588-1063 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takahashi M.
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                                                               WARIANTS G-618; 632-DVR-634; G-634; MEDLINE-93275414; PubMed-8099202;
                                                                                                                                                   "Mutations
                                                                                                                                                                Donis-Keller H., Dou S., Chi D., Carlson K.M., To Lairmore T.C., Howe J.R., Moley J.F., Goodfellow
                                                                                                                                                                                                                                                                                 "Mutations of the RET proto-oncogene in the multiple endocrine neoplasia type 2 syndromes, related sporadic tumours, and
                                                                                                                                                                                                                                                                                                                  MEDLINE-97220587; p
Eng C., Mulligan L.
                                                                                                                                                                                                                                                                                                                                                  REVIEW ON VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                "Mutations in Hirschsprung
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98023959;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ret transforming
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15-JUN-2002
     'Germ-line
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and expression of the ret proto-oncogene
ith two potential transmembrane domains.";
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   mutations
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                                                                                                                  2:851-856(1993)
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einga J., Buys C.
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41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                   PubMed=9067749;
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disease:
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   Romeo G., Ronchetto P., Luo Y., Barone V., Seri
Pasini B., Bocciardi R., Lerone M., Kaarliane
"Point mutations affecting the tyrosine kinase
proto-oncogene in Hirschsprung's disease.";
                                                               VARIANTS HSCR PRO-765; GLN-897 AN MEDLINE=94159103; PubMed=8114938;
                                                                                                                                                                Stelwagen T., Luo Y., Pasini B., Hoer Romeo G., Lips C.J.M., Buys C.H.C.M., "A mutation in the RET proto-oncogene
                                                                                                                                                                                                                                                                                               "Diverse phenotypes proto-oncogene.";
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95187155; PubMed-7881414;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neoplasia type 2A.";
Nature 363:458-460(1993).
                                                                                                                                                                                                                Hofstra R.M.W.,
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Mol. Genet. 3:1
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endocrine
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Yin L. Barone V., Seri M., Bolino A., Bock Pasini B., Tocco T., Lerone M., Cywes S., I Vanderwinden J.-M., Abramowicz M.J., Kristk Hamel B.C.J., Silengo M., Martucciello G., "Heterogeneity and low detection rate of R Mulligan L.M., Eng C., Attie T., Lyonne Robinson B.G., Frilling A., Verellen-Du Venter D.J., Munnich A., Ponder B.A.J.; MEDLINE-95219414; PubMed-7704557; cker I., Billaud M., Calender A., C., Modigliani E., Lenoir G.M.; C-oncogene mutations in French ME Genet. 3:1939-1943(1994). Maurer L.H., Memoli V.A., proto-oncogene associated
pe 2B and sporadic medullar Verellen-Dumoulin HSCR/MEN2A R-618, Ceccherini I., Hoeppener J.W. Lyonnet inherited F-620; Nagai G.F., GLY-972 Y.J., kinase exon Kristoffersson U., I., Noll W. neoplasia SER-618 Bocciardi MEN s. RET M.A., Healey Jackson C.E., Q-897; G-972 AND L-973 10 R-620; medullary Nutile-Mcmenemy Ball D.W., Baylin Moore Chambe Seri M., and domain of Romeo mutations 2A mutations Marsh n C., s AND AND . : their H., Martucciel domain of the and sporadic medullary type F-634; Š Stulp R.P., '. . with multiple в., Safar VARIANT HSCR/FMTC thyroid D.J., EMTC van f the 2B ar Ceccherini detection Ceccherini C.S., , Tunnacliffe of the Ginet N., G-634 and in Amstel families."; Larsson L.T., Hyland Hirschsprung related S.B., 5 H.R. γģ ?

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Edery P., Lyonnet S., Mulligan L.M.,
Holder S., Nihoul-Fkete C., Ponder B.
"Mutations of the RET proto-oncogene
"Mutations of the RET proto-oncogene
Nature 367:378-380(1994).
                                                                                                                            VARIANT FMTC ASP-768. MEDLINE=95148221; Pul Eng C., Smith D.P., N
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Leukocyte;
MEDLINE=96090258; PubMed=7581377;
Attie T., Pelet A., Edery P., Eng C., Mulligan L.M., Amiel J.,
Boutrand L., Beldjord C., Nihoul-Fekete C., Munnich A., Ponder
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Carlson K.M., Dou S., Chi D., Scavarda N., Toshima K., Jackson C.E.,
Wells S.A. Jr., Goodfellow P.J., Donis-Keller H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 367:377-378(1994).
[16]
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Buys C.H.C.M., Cass D.T., Chakravarti A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takami H., Hikiji K., Nakamura Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colomer A., Roth J., Heitz P.U.;
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                                                                                                                                                                                                                                                        VARIANT MEN2B THR-918, AND VARIANT TYR-922.
MEDLINE-96121602; PubMed-8595427;
Kitamura Y., Scavarda N., Wells S.A. Jr., Jackson
                                                                                                                                                                                                                                                                                                                                            "Diversity of RET proto-oncogene mutations in familial and sporadic Hirschsprung disease.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Blood;
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Takami H., Hikiji K., Nakamura
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                                                                                                                                                                                           "Two maternally derived missense mutations in the tyrosine kinase domain of the RET protooncogene in a patient with de novo MEN 2B."; hum. Mol. Genet. 4:1987-1988(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease.";
                                                                                                                                                                                                                                                3oodfellow P.J.;
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                            62 EKACFMSHAVLWEQALDEGVPYIA----VFED----DVLLGEGAEQFLAEDTWLQERFDP 113
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ERALTMGDLISFAWQISQGMQYLAEMKLVHRDLAARNILVAEGRKMKISDFGLSRDVYEE
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                                                                                                                              Mulligan L.M.,
                                                                              5.7%;
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                                                               Score 83.5; D
Pred. No. 12;
52; Mismatches
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                                                                                                                              Healey C.S.,
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I.A.J., Munnich A.;
in Hirschsprung's disease.";
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                                                                                           DB 1;
                                                                67;
                                                                                                                              Zvelebil M.J.,
                                                                                           Length 1114;
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Mol. Microbiol. 36:1059-1070(2000).
EMBL; AF121135; AAF14360.1;
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Q93EK5;
Q1-DEC-2001
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                                                                                                                                                                                                                                         Zhu P., Klutch M.J., Tsai C.-M.;
"Genetic Analysis of Conservation and Variation of Lipooligosaccharide Expression in Two L8-Immunotype Strains of Neisseria meningitidis.";
FEMS Microbiol. Lett. 203:173-177(2001).
EMBL; AF355193; AAL12841.1;
Interpro; IPR002654; GT_25.
Pfam; PF01755; Glyco_transf_25; 1.
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Bacteria; Proteobacteria;
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EMBL; AF240672; AAG09765.1; -. InterPro; IPR002654; GT_25.
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NCBI_TaxID=28449;
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Submitted (OCT-2000) to the EMBL/(EMBL; AF313394; AAK70340.1;
InterPro; IPR002654; GT_25.
Pfam; PF01755; Glyco_transf_25; 1
  Q9REX4;
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01-MAY-2000
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Bacteria; Proteobacteria;
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LGTE.
Neisseria gonorrhoeae.
Macteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                     MEDLINE=20305049; PubMed=10844691;
Harvey H.A., Porat N., Campbell C.A.,
Phillips N.J., Apicella M.A., Balke M.
"Gonococcal lipooligosaccharide is a l
"ecceptor on human sperm.";
Mol. Microbiol 36:1059-1070(2000).
EMBL; AF121135; AAF14363.1;
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Balthazar J.T., Sh
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01-MAR-2002
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EMBL; AF208063; AAF20992.1; -.
InterPro; IPR002654; GT_25.
Pfam; PF01755; Glyco_transf_25;
SEQUENCE 280 AA; 32448 MW; /
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                                              Transferase
                                                  Pfam; PF01755; Glyco_transf_25;
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                                                                                                                                                                       Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
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Score 1002.5; DB 2; Pred. No. 1.1e-83; 3; Mismatches 40;
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                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21467954; pubMed-11583844;
Zhu P., Klutch M.J., Tsai C., M.;
"Genetic Analysis of Conservation and Variation of Li
Expression in Two L8-Immunotype Strains of Neisseria
FEMS Microbiol. Lett. 203:173-177(2001).
EMBL; AL162753; CAB83819.1; -.
EMBL; AF355194; AA112844.1; -.
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STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis (serogroup A),
Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivi
NCBI_TaxID-65699, 487;
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Pred. No. 3e-8
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Q9EVD3;
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280 AA;
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Pfam; PF01755; Glyco_transf_25;
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lipopolysaccharide immunotypes in
Microbiology 145:3013-3021(1999).
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MEDLINE-20055626; PubMed-10589709;
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01-MAR-2002
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01-MAY-1997
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Bacteria; Proteobacteria;
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67.1%;
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Pred. No. 1.8
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RESULT 11
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Matches 191
                      Query Match
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    Matches
                                                               Zhu P., Klutch M.J., Tsai C.-M.;

Zhu P., Klutch M.J., Tsai C.-M.;

"Genetic Analysis of Conservation and Variation of Lipooligosaccharide Expression in Two L8-Immunotype Strains of Neisseria meningitidis.";

FEMS Microbiol. Lett. 203:173-177(2001).

EMBL; AF35519; AALI2842.1; -.

InterPro: IPR002654; GT_25.

InterPro: IPR002654; GT_25.

Pfam; PF01755; Glyco_transf_25; 1.

SEQUENCE 280 AA; 32898 MW; 504256FF55D92F97 CRC64;
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01-DEC-2001
01-MAR-2002
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Galactosyl t
LGTE.
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Bacteria; Proteobacteria;
MCBI_TaxID=487;
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Bacteria; Proteobacteria;
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"Analysis of lipooligosaccharide biosynthesis
J. Bacteriol. 183:934-941(2001).
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18; Conservative
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Pred. No. 3.5
                                          Score 912.5;
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01-JUN-2002
01-JUN-2002
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"Identification of LOS biosynthesis gene lic2B as a putative 'factor in strains of non-typeable Haemophilus influenzae that otitis medi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases EMBL, AY091470; AAM12037.1;
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Bacteria; Proteobacteria;
Haemophilus
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SEQUENCE 266 AA;
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Matches
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01-MAY-1999
01-MAY-1999
01-MAR-2002
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J. Bacteriol. 182:2292-2298(2000).
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Bacteria; Pı
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01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                         Haemophilus somnus
Bacteria; Proteoba
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                  Wu Y., McQuiston J.H., Cox A., Pack T.D., Inzana My Y., McQuiston J.H., Cox A., Pack T.D., Inzana My Molecular cloning and mutagenesis of a DNA loculipooligosaccharide biosynthesis in Haemophilus Infect. Immun. 68:310-319(2000).

EMBL; AF09697; AAC83803.1; ...
                                                                                                                    NCBI_TaxID=731;
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Pfam; PF01755; Glyco_transf_25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-35000HP;
                                                                        MEDLINE=20072700; PubMed=10603403;
                                                                                               SEQUENCE FROM N.A.
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           IPR002654;
                                                                                                                                          Proteobacteria;
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Glyco_transf_25;
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01-JUN-2001
01-MAR-2002
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                                                                                                                                                                                                                                                    InterPro; IPR002654; GT_25.
pfam; pF01755; Glyco_transf_25;
Hypothetical protein; Complete ;
SEQUENCE 208 AA; 24649 MW;
                                                                                                                                                                                                                                                                                                    May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam "Complete genomic sequence of Pasteurella multocida Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AE006155; AAK03225.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical PM1141.
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SEQUENCE 282 AA;
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May B.J., Zhang Q., Li L.L., Paust
                                                                                                                                                                                                                                                                                                                                                                 STRAIN-PM70;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Pasteurella
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                                                              DDREGMPVCQLNPALCAQELHYAKFHDQNSALGSLIEHDR-----
                                                                                                               --PSGVADYGGRAFPLLESEHCGTAGYIISRKAMRFFLDRFAVLPPERLHPVDLMMFGNP 189
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                                                                                               ALPNPVS-YCGRDFLALKDEHLGTAGYIISLGAAKYLLEIFKNMESNNIFPIDHLIFNRF
                                                                                                                                                MWHKCIQDNLPYIAIFEDDILLGRDARTFLAEDEWLESRENCDDIFIIRLETFLQETICE 60
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                      NTFKHRLIRALTKIGREREKRRORRE---
                                                LAGEELMVYQLSPALCIQEL ---
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                                                                                                                                                                                                  ch 23.9%;
l Similarity 37.3%;
82; Conservative '
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2 (TREMBLIEL 20, 1
11 protein PM1141.
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35.5%;
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                      QLIGKIIVPFQ
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No. 4.7e-24;
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